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(54) **Title: DNA SEQUENCES FOR ENZYMATIC SYNTHESIS OF POLYKETIDE OR HETEROPOLYKETIDE COMPOUNDS**
(54) **Titre: SEQUENCES D'ADN DESTINEES A LA SYNTHESE ENZYMATIQUE DE COMPOSES A BASE DE POLYKETIDES OU D'HETEROPOLYKETIDES**

(57) Abstract

The invention consists of: (1) cloned Sorangium cellulosum polyketide synthase (PKS) biosynthetic cluster DNA; and (2) the nucleotide sequence and predicted protein coding sequences of the cloned DNA. The invention can be used for, but not limited to: (a) increasing yields of PKS product in Sorangium cellulosum (e.g., by amplification or genetic modification of the epothilon gene cluster or its component parts); (b) increasing yields of polyketide product in a heterologous system by transfer of the epothilone gene cluster or its component parts, which may be followed by amplification or genetic modification of the PKS gene cluster or its component parts; (c) modification of the polyketide product chemical structure in either Sorangium cellulosum or a heterologous host (e.g., by genetic modification of the epothilone gene cluster or its component parts; and (d) for the detection of genes and gene products involved in making polyketides or related molecules in other organisms (e.g., by hybridization or complementation assays). DNA sequence and analysis is presented for the following cosmids and plasmids: A2 cosmid; the pEPOcos6 region (overlapping of pEPOcos6 and pEPOcos7); pEPOcos8 cosmid; A5 cosmid; Sau4 (10 kb plasmid).

(57) Abrégé

L'invention concerne: (1) un ADN biosynthétique cloné en grappe de polykétide synthase (PKS) de Sorangium cellulosum; et (2) la séquence nucléotidique et les séquences protéiques codantes prévues de l'ADN cloné. L'invention peut avoir les applications suivantes (sans caractère limitatif): (a) augmentation de la production de PKS chez Sorangium cellulosum (p.ex., par l'amplification ou la modification génétique de la grappe de gènes épothilone ou de ces parties constitutives); (b) augmentation de la production du produit polykétide dans un système hétérologue par le transfert de la grappe de gènes épothilone ou de ces parties constitutives, qui peut être suivie par l'amplification ou la modification génétique de la grappe de gènes PKS ou des ses parties constitutives; (c) modification de la structure chimique du produit polykétide soit chez Sorangium cellulosum soit chez un hôte hétérologue (p.ex., par l'amplification ou la modification génétique de la grappe de gènes épothilone ou de ces parties constitutives); et (d) détection de gènes et de produits géniques participant à la fabrication de polykétides ou de molécules correspondantes dans d'autres organismes (p.ex., par des dosages à hybridation ou à complémentation). La séquence d'ADN et l'analyse sont présentées pour les cosmides et les plasmides suivants: cosmide A2; région pEPOcos6 (se chevauchant avec pEPOcos6 et pEPOcos7); cosmide pEPOcos8; cosmide A5; Sau4 (plasmide 10 kb).

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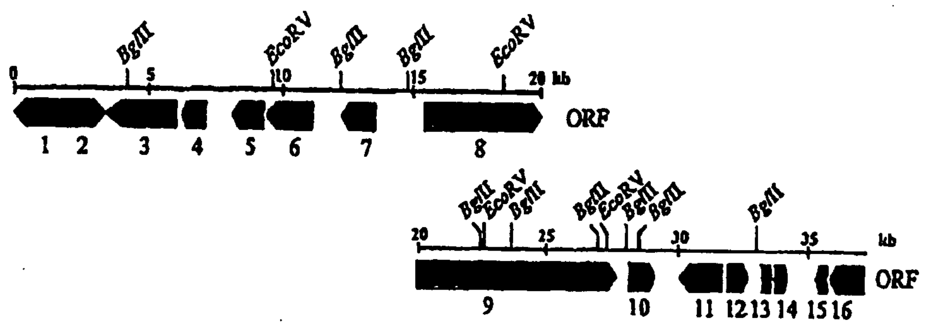

(57) Abstract

The invention consists of: (1) cloned *Sorangium cellulosum* polyketide synthase (PKS) biosynthetic cluster DNA; and (2) the nucleotide sequence and predicted protein coding sequences of the cloned DNA. The invention can be used for, but not limited to: (a) increasing yields of PKS product in *Sorangium cellulosum* (e.g., by amplification or genetic modification of the epothilone gene cluster or its component parts); (b) increasing yields of polyketide product in a heterologous system by transfer of the epothilone gene cluster or its component parts, which may be followed by amplification or genetic modification of the PKS gene cluster or its component parts; (c) modification of the polyketide product chemical structure in either *Sorangium cellulosum* or a heterologous host (e.g., by genetic modification of the epothilone gene cluster or its component parts; and (d) for the detection of genes and gene products involved in making polyketides or related molecules in other organisms (e.g., by hybridization or complementation assays). DNA sequence and analysis is presented for the following cosmids and plasmids: A2 cosmid; the pEPOcos6 region (overlapping of pEPOcos6 and pEPOcos7); pEPOcos8 cosmid; A5 cosmid; Sau4 (10 kb plasmid).

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Description

DNA sequences for enzymatic synthesis of polyketide or heteropolyketide compounds

The present invention relates to DNA sequences for enzymatic synthesis of polyketide or heteropolyketide compounds produced by the bacterium *Sorangium cellulosum*.

Background and introduction

This patent application describes DNA sequences for the enzymatic synthesis of polyketide and/or heteropolyketide structures synthesized by the myxobacterium *Sorangium cellulosum*. Several of these compounds have known cytotoxic, immunosuppressive, antibiotic and fungicidal biological activity, with the epothilones having been most studied and characterized. The fermentation of large quantities of secondary metabolites from microorganisms, especially from myxobacteria, is a time consuming and difficult process that often involves complications (e.g. contamination, low product yield, difficult isolation and purification). Therefore it would be advantageous to use a well-characterized organism for such fermentations. After cloning of the desired biosynthetic genes one could create such an organism via genetic engineering and manipulate the biosynthesis of the compound. Identified sequences can be cloned into optimized expression vectors and generate recombinant cell lines that overproduce polyketide structures.

Polyketide synthases (PKS) and non-ribosomal peptide synthetases (NRPS) represent macromolecular and multifunctional enzymes which are characterized by a modular architecture. PKS condenses activated carbonic acids (usually acetate and propionate) and reduce the resulting 2-keto acid intermediates stepwise in a fatty acid biosynthesis-like fashion. Responsible for each reaction step is a specific domain that recognizes, activates, condenses and reduces the carbonic acid. Depending on the presence of these domains in the corresponding modules, every reduction stage can occur in the final product (Rawlings, Nat. Prod. Reports <u>14</u>, 523-556 [1997]; for a review, see Chem. Rev. <u>97</u>, 2463-2760 [1997]). A typical example for the biosynthesis of a polyketide is the macrolide antibiotic erythromycin (Staunton and Wilkinson, Chem. Rev. <u>97</u>, 2611-2630 [1997]). NRPSs are also modular enzymes and condense via peptide bonds amino acids to low molecular weight bioactive substances like bacitracin or tyrocidin. Typical domains of these systems activate the amino acid and condense it with the growing peptide chain. Methylations, epimerisations and modifications via additional protein domains are possible (Stachelhaus and Marahiel, FEMS Microbiol Lett. <u>125</u>, 3-14 [1995]). Both types of enzymes (NRPS and PKS) share the modular organization of the proteins in which specific catalytic domains are responsible for recognition, activation, condensation and modification of the single elongation units. The growing chain of amino acids and/or carbonic acids is extended through the action of one module adding one unit. The domains of each module carry the active centers responsible for the enzymatic steps of the biosynthesis.

Little is known about the biosynthesis of biologically active polyketides and polypeptides from myxobacteria. Fragments of the biosynthetic gene clusters of soraphen and saframycin have been described from *Sorangium cellulosum* So ce26 and *Myxococcus xanthus*, respectively (Schupp et al., J. Bacteriol. 177, 3673-3679 [1995] and Pospiech et al., Microbiology 141, 1793-1803 [1995]). We have constructed genomic libraries of the epothilone producer *Sorangium cellulosum* So ce90. Gene probes based on PKS and PS genes were used to isolate recombinant cosmids, which were then sequenced and characterized. Several unique pathways containing PKS, PS, or a combination of both types of genes were identified, demonstrating that this organism is potentially a rich source of novel bioactive compounds.

A subject of the present invention is therefore to provide DNA sequences according to claim 1 the expression products of which perform or are involved in the enzymatic biosynthesis, mutasynthesis or partial synthesis of polyketide or heteropolyketide compounds. The DNA sequences may be inserted into well known and optimized expression vectors by commmon techniques of molecular biology, thus allowing transformation, selection and cloning of cells, which cells are then capable of synthezising polyketide or heteropolyketide compounds by fermentation. Using an overproducing clone allows the desired polyketide or heteropolyketide compounds be easily produced and recovered in high amounts. Further, knowledge of the localization of regulatory DNA segments and individual structural genes allows "site-directed mutagenesis" using common techniques for genetic engineering, and thus construction of optimized enzymes ("protein engineering") for fermentative synthesis of polyketide or heteropolyketide compounds.

The invention thus further relates to a recombinant expression vector according to claim 16, cells transformed therewith according to claim 17 and to a process for enzymatic biosynthesis, mutasynthesis or partial synthesis of polyketide or heteropolyketide compounds according to claim 23.

Preferred and/or advantageous embodiments of the present invention are subject-matter of the subclaims.

In brief, the invention consists of (1) cloned *Sorangium cellulosum* polyketide synthase (PKS) and/or peptide synthetase (PS) biosynthetic cluster DNA and (2) the nucleotide sequence and predicted protein coding sequences of the cloned DNA. The invention can be used for, but not limited to, (a) increasing yields of PKS product in *Sorangium cellulosum* (e.g., by amplification or genetic modification of the epothilone gene cluster or its component parts), (b) increasing yields of polyketide and/or peptide synthetase product in a heterologous system by transfer of the corresponding gene cluster or its component parts, which may be followed by amplification or genetic modification of the PKS and/or PS gene cluster or its component parts, (c) modification of the polyketide and/or peptide synthetase product chemical structure in either *Sorangium cellulosum* or a heterologous host (e.g., by genetic modification of the corresponding gene cluster or its component parts) and (d) for the detection of genes and gene products involved in making polyketides or related molecules in other organisms (e.g., by hybridization or complementation assays). DNA sequence and analysis is presented for the following cosmids and plasmids:

- A2 cosmid as defined in claim 6
- the pEPOcos6 region (overlapping of pEPOcos6 and pEPOcos7) as defined in claim 7

- pEPOcos8 cosmid as defined in claim 10
- A5 cosmid as defined in claim 12
- Sau4 (10 kb plasmid) as defined in claim 14

The invention is now described in more detail by examples and for illustration only. The examples are not to be construed as any limitation of the scope.

Figure 1 is a restriction map of one of the DNA sequences of the present invention (cosmid A2 insert) indicating also the localization of regulatory DNA segments and the individual structural genes ("open reading frames" or ORFs) 1 to 16.

Figure 2 shows the open reading frames found on pEPOcos6 region

DNA sequence data from A2 cosmid are as defined in claim 6.

Table 1 correlates ORFs 1 to 16 found on A2 cosmid with the respective biological function (Regulators, Enzymes).

Table 1

	gene/function	position
ORF 1	regulatory element	1666 - 1
ORF 2	regulatory element	1605 - 3338
ORF 3	acyl-t-RNA synthetase	6100 - 3398
ORF 4	monooxygenase	7110 - 6374
ORF 5	amino transferase	9590 - 8433
ORF 6	L-dopa decarboxylase	11393 - 9855
ORF 7	oxidoreductase	13656 - 12712
ORF 8	polyketide synthase	15374 - 18984
ORF 9	polypeptide synthetase	20003 - 27889
ORF 10	peptidase	28251 - 29402
ORF 11	regulatory element	31720 - 30401
ORF 12	sigma factor	31982 - 32932
ORF 13	regulatory element	33128 - 33613
ORF 14	regulatory element	33661 - 34007
ORF 15	transcription regulator	35611 - 35255
ORF 16	signal transduction	37856 - 35730

Working Examples

A. Construction of a *Sorangium cellulosum* cosmid library

1. Isolation of genomic DNA from *S. cellulosum* So ce90

a. *Sorangium cellulosum* So ce90 was spread onto solid CA-2 agar and incubated at 30°C for 5-7 days. CA-2 agar is prepared by autoclaving 18 g Bacto-agar (Difco Laboratories, Detroit, MI) in 800 ml dH_2O for 20 min at 121°C and cooling to 50-55°C in a water bath. The following filter-sterilized solutions are added to the agar: 20% (w/v) glucose, 50 ml; Solution A (7.5% [w/v] KNO_3, 7.5% K_2HPO_4), 10 ml; Solution B (1.5% [w/v] $MgSO_4 \cdot 7H_2O$), 10 ml; Solution C (0.2% [w/v] $CaCl_2 \cdot 2H_2O$, 0.15% [w/v] $FeCl_3$), 10 ml; 1 M HCl, 1 ml; autoclaved 4-day old *Sorangium cellulosum* broth, 100 ml. A sample of cells was removed from the plates with a sterile loop and inoculated into 50 ml of G51t medium in a 250 ml Erlenmeyer flask. G51t consists of 0.5% starch (Cerestar), 0.2% tryptone, 0.1% yeast extract, 0.05% $CaCl_2$, 0.05% $MgSO_4 \cdot 7H_2O$, 1.2% 4-(2-hydroxyethyl)-1-piperazine-ethanesulfonic acid (HEPES), 0.2% glucose, pH 7.6. The flasks were shaken at 30°C, 160 rpm until a dense orange bacterial growth was obtained (ca. 5-7 d.). The cells were pelleted by centrifugation at 6,000 x g and used immediately or stored frozen at -20°C.

The protocol used for isolating chromosomal DNA from bacteria using hexadecyltrimethylammmonium bromide (CTAB) has been described previously (Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1990). The precipitated DNA was recovered with a bent Pasteur pipette, washed with 70% and 95% ethanol, air-dried, and resuspended in 0.5 ml TE buffer (0.01 M Tris-HCl, 0.001 M ethylenediaminotetraacetic acid [EDTA], pH 8.0).

b. Alternatively, genomic DNA was isolated from *S. cellulosum* cells cultured as described in section A.1 using the Midi Qiagen Blood & Cell Culture DNA purification Kit (Qiagen, Hilden, Germany) following the Qiagen Genomic DNA Handbook protocol for bacterial DNA isolation (1997, Qiagen, Hilden, Germany, p. 29 ff.). In order to obtain high molecular weight chromosomal DNA the precipitated DNA was recovered with a bent pasteur pipette as described in section A.1.

2. Isolation of plasmid DNA

a. pFD666: pFD666 is a bifunctional *E. coli-Streptomyces* cosmid cloning vector (see Denis and Brzezinski, Gene 111, 115-118 [1992]). To maintain stability of large inserts, it is present in low-medium copy number when replicated in *E. coli*. For this reason, isolation of sufficient pure DNA to carry out cloning experiments was difficult using commercial kits with standard protocols. A modified procedure was therefore used to obtain pFD666 DNA. A 10 ml culture of DH10B(pFD666) was grown for 16-20 hr at 37°C in LB (1% tryptone, 0.5% yeast extract, 0.5% NaCl, pH 7.0) medium containing 50 µg/ml kanamycin sulfate. Fifty ml of LB + kanamycin was inoculated to a starting OD_{600} of ca. 0.25 and shaken at 300 rpm, 37°C, until the OD_{600} reached ca. 0.6. Five hundred ml of LB + kanamycin medium in a 2 l flask was inoculated with 25 ml of this culture and incubated under the same conditions for 2.5 hr. Chloramphenicol (2.5 ml of a 34 mg/ml solution in 100% EtOH) was added and the incubation continued for an additional 16-20 hr. (The previous steps were performed according to Maniatis et al. Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989.) Cells were pelleted for 10 min, 16,000 x g . They were resuspended in 9 ml of 50 mM glucose/25 mM Tris-HCl (pH 8.0)/10 mM EDTA and transferred to a 50 ml disposable centrifuge tube. One ml of a freshly-prepared 10 mg/ml lysozyme solution in 10 mM Tris-HCl, pH 8.0 was added and the cell suspension incubated in a 37°C water bath for 10 min. Twenty ml of a freshly-prepared 0.2 NaOH/1% sodium dodecyl sulfate (SDS) solution was added and the tube inverted gently 5-7 times to mix the contents. After 5 min at room temperature, 15 ml of 5 M potassium actate (pH 4.8) was added and the tube inverted sharply 3-4 times. The tube was centrifuged at 6,000 x g for 10 min at 4°C and the supernatant poured though 2 layers of sterile cheese cloth into a fresh 50 ml disposable tube. Isopropanol to a final concentration of 0.6% was added and the contents of the tube mixed several times. The precipitated nucleic acid was centrifuged at 6,000 x g for 10 min at 4°C. The pellet was washed with 70% EtOH and any excess EtOH was aspirated from the pellet, which was allowed to air dry for 5 min. It was resuspended in 5 ml of 50 mM 3-(N-Morpholino)propanesulfonic acid (MOPS)/750 mM NaCl, pH 7.0 and added to an equilibrated to QIAfilter Midi column (Qiagen, Chatsworth, CA). The manufacturer's protocol for washing and eluting the plasmid DNA was followed.

b. **SuperCos:** SuperCos plasmid DNA was purchased from Stratagene (La Jolla, CA).

3. Preparation of ca. 38-47 kb *Sau*3A1 fragments of *S. cellulosum* chromosomal DNA

a. *S. cellulosum* chromosomal DNA prepared as described in section A.1.a was partially cleaved with restriction endonuclease *Sau*3A1 in a 1000 μl reaction volume consisting of 50 μg chromosomal DNA, 5 units enzyme (Promega, Madison , WI), 0.006 M Tris-HCl, 0.006 M $MgCl_2$, 0.10 M NaCl, and 0.001 M dithiothreitol (pH 7.5) for 5 min at 37°C. The reaction mixture was extracted once with an equal volume of 1:1 phenol:chloroform. After centrifugation, the upper aqueous phase was saved, to which 0.1 vol. of 3 M sodium acetate and 0.6 vol. isopropanol was added. DNA was pelleted by centrifugation for 5 min at 16,000 x g in a microfuge and washed once with 0.5 ml 70% EtOH. After drying in a SpeedVac (Savant Instruments, Farmingdale, NY) for 5 min, the pellet was resuspended in 0.1 ml TE buffer. The DNA was layered ontop of a 12 ml 10-40% sucrose gradient prepared in TE buffer and centrifuged at 113,600 x g for 16 hr, 10°C using a Beckman SW40Ti rotor (Beckman Instruments, Palo Alto, CA). Five hundred μl aliquots of the gradient were removed using a pipetor beginning at the top of the tube. Samples (5 μl) of the fractions were analyzed by electrophoresis through a 0.5% agarose gel in TAE buffer (0.04 M Trizma base, 0.02 M acetic acid, and 0.001 M EDTA, pH 8.3) containing 0.5 μg/ml ethidium bromide for 6 hr at 100 V. Fractions containing DNA fragments of ca. 40-45 kb were identified by comparison to a high molecular weight DNA standard (Life Technologies, Gaithersburg, MD). Sucrose was diluted from the corresponding 0.5 ml fraction by addition of 0.5 vol. TE. Subsequently, DNA was precipitated by addition of 0.1 vol. 3 M sodium acetate and 0.6 vol. isopropanol. DNA was pelleted by centrifugation at 16,000 x g for 10 min in a microfuge. DNA was washed with 0.5 ml 70% EtOH and dried in a SpeedVac with moderate heat for 10 min. Finally, the DNA was resuspended in distilled H_2O at a concentration of 0.5 mg/ml.

b. Alternatively, 10 µg of *S. cellulosum* chromosomal DNA prepared as described in A.1.b was treated with 0.3 U *Sau*3A1 (New England Biolabs, Beverly, MA) for 1 h at 37°C in 400 µl of the supplier's recommended reaction buffer. Formation of DNA fragments of about 40 kb in size was checked by comparison of the motility behavior with high molecular weight DNA standards after a 0.3% agarose gel electrophoresis. An equal volume of phenol:chloroform (1:1) was added, mixed and centrifuged. The upper aqueous phase was recovered and 0.1 vol. of 3 M sodium acetate and 0.6 vol. of isopropanol were added. After centrifugation, the precipitated DNA was washed twice with 0.5 ml 70% ice cold ethanol and finally air-dried. The DNA fragments were resuspended in 100 µl shrimp alkaline phosphatase reaction buffer and dephosphorylated for 150 min. at 37°C using 2 U shrimp alkaline phosphatase (Amersham Life Science, Cleveland, OH). A phenol:chloroform extraction followed as described above. Finally, the DNA was precipitated by addition of 0.1 vol. 3 M sodium acetate and 0.6 vol. isopropanol, dried, and dissolved in TE buffer.

4. Preparation of cosmid libraries

a. Using pFD666: Vector pFD666 was cleaved with restriction endonuclease BamHI in a 0.02 ml reaction volume consisting of 2 μg plasmid DNA, 10 units of BamHI (Promega), 0.006 M Tris-HCl, 0.006 M $MgCl_2$, 0.05 M NaCl, and 0.001 M dithiothreitol (pH 7.5) for 90 min at 37°C. Five μl of 10x alkaline phosphatase buffer (0.5 M Tris-HCl [pH 9.3], 0.01 M $MgCl_2$, 0.001 M $ZnCl_2$, 0.01 M spermidine) was added to the reaction followed by alkaline phosphatase (0.01 units/pmol ends; Promega) and distilled H_2O to a final volume of 0.05 ml. The sample was incubated for 30 min at 37°C and a second aliquot of phosphatase was added. After a further 30 min at 37°C, 0.3 ml of stop buffer (0.01 M Tris-HCl [pH 7.5], 0.001 M EDTA, 0.2 M NaCl, 0.5% SDS) and 0.35 ml of 1:1 phenol; $CHCl_3$ was added to the reaction. The sample was mixed gently several times by inversion and centrifuged at 16,000 x g for 3 min to separate the phases. The aqueous layer was removed to a new microfuge tube. 0.1 vol. 3 M sodium acetate and 2 vol. 100% EtOH were added and the precipitated DNA pelleted by centrifugation at 16,000 x g for 10 min. Liquid was removed by aspiration and the pellet washed once with 0.5 ml 70% EtOH. The DNA was dried in a SpeedVac and resuspended in TE buffer to 0.5 mg/ml.

Digested, phosphatase-treated pFD666 was ligated to the partially-cleaved chromosomal DNA (see sections A.3.a and B.1.a) in a 0.005 ml reaction consisting of 1 μg pFD666, 1 μg *S. cellulosum* DNA, 0.03 M Tris-HCl (pH 7.8), 0.01 M $MgCl_2$, 0.01 M dithiothreitol, and 0.0005 M adenosine-5′-triphosphate and 1.5 Weiss units of T4 DNA ligase (Promega). The reaction was carried out at room temperature for 2 hr. The entire reaction mix was packaged into bacteriophage λ *in vitro* using Packagene extracts (Promega) according to the manufacturer's directions. The entire packaging reaction (0.5 ml) was diluted with 4.5 ml SM buffer (per liter: 5.8 g NaCl, 2 g $MgSO_4.7H_20$, 1 M Tris-HCl[pH 7.5], 5 ml 2% gelatin solution). Transfection was performed by adding 10 ml of an overnight culture of *E. coli* DH5α that had been grown in LB medium with 0.01 M $MgSO_4$ and 0.2% maltose to the diluted phage and incubating at 37°C for 20 min. 0.8 ml of LB was added and the cells shaken at 225 rpm for 1 hr at 37°C. Cells were pelleted, resuspended in LB, and spread onto a 150 mm LB + kanamycin agar plate. After 3 d. at 30°C, the colonies were harvested by picking ca. 800 colonies into 2.0 ml LB + kanamycin medium containing 20% glycerol, freezing on dry ice, and storing at -70°C. In addition, six kanamycin-resistant colonies were inoculated into 2 ml LB + kanamycin liquid medium and incubated at 37°C, 250 rpm, for 18-24 hr. Cosmid DNA was prepared using a standard alkaline lysis procedure starting with 1.5 ml of the culture. DNA was digested with restriction endonuclease PstI and samples electrophoresed on a 0.8% TAE agarose gel for 1.5 hr at 100 V. A unique restriction pattern was noted in each sample and the total size of the insert was calculated to be between 40 and 45 kilobases.

b. Using SuperCos: 30 μg of vector SuperCos was digested with XbaI (New England Biolabs, Beverly, MA) for 210 min at 37°C in 100 μl of the recommended reaction buffer. Ten μl sodium acetate and 60 μl isopropanol was added before the solution was centrifuged for 30 min at 16,000 x g. The precipitated DNA was washed twice with 500 μl ice cold 70% ethanol. The vector DNA was precipitated and air-dried, dissolved in 135 μl shrimp alkaline phosphatase reaction buffer and treated with 2.5 U shrimp alkaline phosphatase for 150 min. After heat inactivation of the enzyme at 75°C for 20 min, a phenol:chloroform extraction was performed as described in section 1. c. The DNA, resuspended in 100 μl BamHI restriction buffer was hydrolyzed with 15 U BamHI (New England Biolabs, Beverly, MA) for 180 min. A phenol:chloroform extraction followed (see section A.3). The SuperCos DNA was precipitated by additon of 0.1 vol 3 M sodium acetate and 0.6 vol isopropanol, centrifuged at 16,000 x g, and resuspended in 50 μl TE buffer.

Four μg of digested vector DNA was ligated with 10 μg partially hydrolyzed genomic DNA from *S. cellulosum* (as described in section A.3.b) in a final volume of 20 μl using 2 U T4 DNA ligase and the appropriate reaction buffer (Gibco BRL, Eggenstein, Germany). The reaction was carried out at 16°C overnight. The reaction mixture was packaged into phage particles using the Gigapack III XL packaging extract kit (Stratagene) according to the manufacture´s protocol. Treatment of packaging reaction mixture and transfection of *E. coli* SURE (Stratagene) was performed as described in 4.a. Transfected cells were concentrated by centrifugation, resuspended in fresh LB medium and distributed on LB agar plates containing 50 $\mu g/ml^{-1}$kanamycin. The plates were incubated overnight at 30°C. 1600 recombinant clones were transferred into 96 well microtiter plates filled with 80 μl LB medium containing 50 μg/ml˙kanamycin per well and propagated overnight at 30°C. The following day the microtiter plates were used to inoculate a second set of microtiter plates in order to obtain a duplicate of the recombinant clones. Each well of the original set of microtiter plates was supplemented with 80 μl 50 % glycerol and the entire plate stored at -70°C.

20 randomly chosen transformants were inoculated into 3 ml LB medium with 50 $\mu g/ml^{-1}$ kanamycin and incubated over night at 37°C in order to isolate plasmid DNA using the Qiagen plasmid extraction kit (Qiagen, Hilden, Germany). Restriction fragment analysis of the recombinant cosmids using the restriction endonucleases PstI and BglII indicated that the cosmids contained inserts of approximately 35 to 42 kb in size.

B. Construction of a *S. cellulosum* plasmid library

1. Preparation of 8-12 kb fragments of *S. cellulosum* chromosomal DNA.

S. cellulosum chromosomal DNA prepared as described in section A.1.a was partially cleaved with restriction endonuclease Sau3A1 in a 100 µL reaction volume consisting of 5 µg chromosomal DNA, 5 units enzyme (Promega, Madison , WI), 0.006 M Tris-HCl, 0.006 M $MgCl_2$, 0.10 M NaCl, and 0.001 M dithiothreitol (pH 7.5) for 4 min at 37°C. The digested DNA was electrophoresed through a 11 x 14 cm 0.8% TAE-agarose gel for 18 hr at 17 V. Fragments of 8-12 kb were cut from the gel and purified using the QIAquick Gel Extraction Kit using the manufacturer's protocol (Qiagen).

2. Preparation of the plasmid library

Plasmid pZero2.1 (Invitrogen, Carlsbad, CA) was cleaved with restriction endonuclease BamHI in a 0.02 ml reaction volume consisting of 1 µg plasmid DNA, 10 units of BamHI (Promega), 0.006 M Tris-HCl, 0.006 M $MgCl_2$, 0.05 M NaCl, and 0.001 M dithiothreitol (pH 7.5) for 20 min at 37°C. 0.08 ml of dH_2O and 0.1 ml of 1:1 phenol:CHCl3 was added. The sample was briefly vortexed and centrifuged at 16,000 x g for 2 min. The aqueous layer was removed to a new microfuge tube. 0.1 vol. 3 M sodium acetate and 2 vol. 100% EtOH were added and the precipitated DNA pelleted by centrifugation at 16,000 x g for 10 min. Liquid was removed by aspiration and the pellet washed once with 0.5 ml 70% EtOH. The DNA was dried in a SpeedVac and resuspended in TE buffer to 0.004 μg/ml. Digested pZero2.1 was ligated to the partially-cleaved chromosomal DNA in a 0.01 ml reaction consisting of 0.004 μg pZero2.1, 0.05 μg *S. cellulosum* DNA, 0.03 M Tris-HCl (pH 7.8), 0.01 M $MgCl_2$, 0.01 M dithiothreitol, and 0.0005 M adenosine-5'-triphosphate and 1.5 Weiss units of T4 DNA ligase (Promega). The reaction was carried out at room temperature for 2 hr. 0.015 ml dH_2O and 0.25 ml of 1-butanol were added, the sample vortexed briefly, and centrifuged at 16,000 x g for 10 min. Liquid was aspirated away from the pellet and the sample dried in a SpeedVac for 5 min. The ligated DNA was resuspended in 0.005 ml dH_2O and mixed with 0.04 ml of electrocompetent *Escherichia coli* DH10B cells (GIBCO/BRL, Gaithersburg, MD). The sample was placed into a pre-chilled 0.2 mm-gap electroporation cuvette and transformed into the bacteria by electroporation using a BioRad Gene Pulser II unit (BioRad, Hercules, CA) at 25 μF and 200 Ω. 0.96 ml SOC medium (0.5% yeast extract, 2% tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM $MgCl_2$, 20 mM $MgSO_4$, 20 mM glucose) was mixed with the cells and transferred to a 1.5 ml microfuge tube. The sample was incubated at 37°C, 225 rpm, for 1 hr. Aliquots of the cells were spread onto an LB agar + kanamycin and incubated at 37°C for 20 hr to estimate the number of transformants obtained. Six kanamycin resistant colonies were confirmed to contain an insert of the expected size as described in section A.4.a.

C. Identification of cosmids possessing polyketide synthase genes

1. Colony blot hybridizations using cosmid library in pFD666: A 20 x 20 cm sheet of Duralon UV membrane (Stratagene) was placed on top of a 24.5 x 24.5 cm square bioassay dish containing 250 ml LB agar - kanamycin. An aliquot of the frozen cosmid library in 1 ml LB medium was spread on the filter. The plate was incubated at 37°C for 24 hr. Colonies were replicated onto two fresh filters which were placed onto LB + kanamycin agar medium and incubated at 28°C for 18 hr. Lysis of cells and neutralization of released DNA was performed according to directions that were provided with the filters. The DNA was crosslinked to the filters using a UV Stratalinker 2400 unit (Stratagene) in the auto crosslink mode. Cell debris was removed by placing the filters in a container with a solution of 3 X SSC (20 X SSC contains, per liter, 173.5 g NaCl, 88.2 g sodium citrate, pH adjusted to 7.0 with 10 N NaOH), 0.1% SDS and rubbing the lysed colonies with a Kimwipe. The filters were then incubated at least 3 hr with the same wash solution for at least 3 hr at 65°C. The plasmid library was treated similarly except cells were spread onto a 137 mm circular Duralon UV membrane placed on top of a 150 mm petri dish containing 80 ml LB agar + kanamycin.

For hybridizations, a probe consisting of a 650-base pair (bp) polymerase chain (PCR) fragment representing a portion of a *S. cellulosum* polyketide synthase gene was used. The fragment was amplified using primers to consensus regions of Type I (macrolide) polyketide synthase (PKS) genes (Swan et al., Mol. Gen. Genetics <u>242</u>, 358-362 [1994]). A series of sense and antisense oligonucleotides were prepared for PCR studies as indicated in the following table 2:

Table 2

Oligo-nucleotide	<u>I. DNA sequence (5'→ 3')</u>	**Corresponding amino acid sequence**
120 (sense)	CGGT(C/G)AAGTC(C/G)AACATCGG	KSNIGHT
121 (anti-sense)	GC(A/G)ATCTC(A/G)CCCTGCGA(A/G)TG	HSQGEIA
122 (sense)	GT(C/G)GACAC(C/G)GC(C/G)TGCTC(C/G)	VDTACSS
123 (sense)	GG(C/G)AC(C/G)AACGC(C/G)CACGT(C/G)AT	GTNAHVI
124 (anti-sense)	CCCTG(C/G)CC(C/G)GGGAA(C/G)ACGAA	FVFPGQG

The selection of C or G where necessary in the third position of a codon reflects the very high overall G + C content of *S. cellulosum* (ca. 70%). Conditions for PCR were as follows: 0.01 M Tris-HCl (pH 9.0), 0.05 M KCl, 0.003 M $MgCl_2$, 0.1% Triton X-100, 200 μM of each primer, 2.5 U Taq DNA polymerase (Promega), 5.0% dimethyl sulfoxide (Sigma), and 0.01 μg of *S. cellulosum* chromosomal DNA in a 0.05 ml reaction volume. Reactions were carried out in a Perkin-Elmer Model 480 Thermocycler (Perkin-Elmer Corporation, Foster City, CA) under the following conditions: 94°C, 1 min; 50°C, 1 min, 72°C, 1.5 min for a total of 30 cycles. Each possible combination of sense and anti-sense primers were tried. A 650-bp and 350-bp fragment was amplified using oligos 120 + 124 and 123 +124, respectively. The sequence of the fragments were determined using the ALFexpress AutoRead kit to fluorescently label the DNA, which was analyzed on an ALFexpress sequencing apparatus (Pharmacia). The data indicated both PCR fragments possessed significant homology to polyketide synthase genes of Type I antibiotics. The 650-bp fragment was chosen for hybridization experiments.

The fragment was labeled with ^{32}P-dCTP using the NEBlot kit (New England Biolabs, Beverly, MA) and purified on a Bio-Spin 6 column (BioRad, Hercules, CA.). Duplicate blots were pre-hybridized in 3 X SSC (1 X SSC contains 0.15 M sodium chloride and 0.015 M sodium citrate, pH 7.0), 4 X Denhardt's solution (100 X is 2% Ficoll [Type 400], 2% polyvinylpyrrolidone, and 2% bovine serum albumin [Fraction V]), and 100 μg/ml sheared, denatured salmon sperm DNA; all reagents purchased from Sigma Chemicals, St. Louis. The labeled DNA was heated in a boiling water bath for 5 min to denature the strands, cooled on ice, and added to the pre-hybridization solution. The filters were incubated for at least 18 hr in a roller bottle hybridization oven. They were transferred to new bottle, then washed two times in 2 X SSC, 0.1% SDS at 70°C for 30 min (moderate stringency). The membranes were placed on Whatman 3MM paper to remove excess liquid, covered with Saran Wrap, and exposed to autoradiography film (Kodak X-OMAT LS) with two intensifying screens. The cassette was placed at -70°C and developed at appropriate intervals.

Approximately 100 colonies were seen to have hybridized on the duplicate filters. Fourteen of these were isolated from the master plate and grown in 4 ml LB + kanamycin medium for 20-24 hr, 37°C, 250 rpm. Plasmid DNA was prepared using the standard alkaline lysis method and digested with restriction endonuclease PstI. The digested DNA was electrophoresed on a 0.8% agarose gel in TAE for 3 hr at 100 V. Fragments were transferred to Duralon UV using the VacuGene XL vacuum blotting unit (Pharmacia) and the recommended alkaline denaturation protocol. Hybridization with radioactively-labeled PCR fragment and washing were carried out as described above. Two prominent types of cosmids were observed; one contained PstI fragments of ca. 7.0, 5.0, and 1.1 kb (pEPOcos6 and pEPOcos7) that hybridized to the probe; the other type had fragments of ca. 6.0 and 3.6 kb (pEPOcos8 and pEPOcos13) which were homologous to the probe. Restriction analysis confirmed that cosmids showing identical hybridization patterns had identical or overlapping inserts. PCR reactions using primers representing consensus sequences of Type I PKS genes were performed using the isolated cosmid DNA as template under conditions described above, except ca. 0.01 μg of cosmid DNA was included as template. Cosmids pEPOcos6 and pEPOcos8 amplified the 650-bp fragment seen when oligonucleotides 120 + 124 were used, while pEPOcos8 and pEPOcos13 supported amplification of an 1100-bp PCR fragment with oligos 122 and 124. The latter fragment was sequenced and confirmed to possess strong similarity to Type I PKS genes. These data confirm that the recombinant cosmids are related to each other and that all contain PKS-like genes.

2. Colony blot hybridizations of plasmid library in pZero2.1:

A 137-mm circle of Duralon UV membrane was placed on top of a 150-mm containing 75 ml LB agar + kanamycin. An aliquot of the plasmid library (representing ca. 2,000 recombinant colonies) in 0.5 ml LB medium was spread on the filter. The plate was incubated at 37°C for 20 hr. Colonies were replicated onto two fresh filters which were placed onto LB + kanamycin agar medium and incubated at 37°C for 6 hr. The filters were processed for hybridization as described in Section C.1. Out of 8 positive colonies detected, one contained a plasmid with a DNA region not encoded by either pEPOcos6 or pEPOcos8. This plasmid, called Sau4, was characterized in more detail.

3. Colony blot hybridizations of cosmid library in SuperCos:

The recombinant *E. coli* clones from the microtiter plates (see section 4. b) were used to produce two identical sets of hybridization filters in order to identify cosmids carrying PKS and PS genes. The recombinant clones were spotted onto 2 sets of 22 x 22 cm LB agar plates containing 50 µg/ml kanamycin. Each plate contained 384 clones therefore representing 4 microtiter plates. The clones were incubated at 30°C overnight. After pre-cooling for approximately 3 h at 4°C, 20 x 20 cm Hybond N^+ Nylon membranes (Amersham, Braunschweig, Germany) were placed onto the agar surfaces. After 2 min. the membranes were removed and placed for 15 min. on Whatman 3 MM paper (Whatman paper Ltd., Maidstone, England) soaked with denaturation solution (0.5 N NaOH, 1,5 M NaCl) before they were transfered onto Whatman 3 MM paper saturated with neutralization solution (1 M Tris-HCl, pH 7.5, 1.5 M NaCl). Subsequently the membranes were placed onto Whatman 3 MM paper soaked with 2 X SSC (0.3 M NaCl, 0.03 M sodium citrate, pH 7.2) for 10 min. The membranes were baked for 40 min at 85°C. Then, each membrane was overlayed with 5 ml Proteinase K solution (2 mg/ml Proteinase K in 2 x SSC) and incubated at 37 °C for 90 min. Finally, cell debris was removed by wiping the membranes with a Kimwipe pre-wetted with 2 X SSC.

As we were seeking in particular to identify biosynthetic pathways containing both PKS and PS genes, the following hybridization strategy was taken: The screening was initially focused on ketosynthase domains from type I PKSs and on the adenylation domain from PSs. Target-specific primers were used to amplify DNA fragments of the corresponding genes from chromosomal DNA of *S. cellulosum* by PCR. The fragments obtained were then cloned, sequenced and the deduced amino acid sequence compared to known ketosynthase and adenylation domains of PKS and PS, respectively. In a second step these PCR fragments were used as gene probes to detect recombinant cosmids of the *S. cellulosum* cosmid library.

Oligonucleotides based on conserved amino acid sequences of ketosynthase domains from various type I PKS were optimized for myxobacterial DNA by comparison to a known myxobacterial biosynthetic gene cluster (Schupp et al., J. Bacteriol. 177, 3673-3679 [1995]) resulting in primer
KS1Up (5´-
C/A)GIGA(A/G)GCI(A/C/T)(A/T)I(C/G)(C/A)IATGGA(C/T)CCICA(A/G)CAI(A/C)G-3´) and
KSD1 (5´-GG(A/G)TCICCIA(A/G)I(G/C)(T/A)IGTICCIGTICC(A/G)TG-3´).
PCR-primers TGD (5´-
T(A/T)(C/T)CGIACIGGIGA(C/T)(C/T)(G/T)IG(G/T)ICG-3´) and

LGG (5´-A(A/T)IGA(A/G)(G/T)(G/C)ICCICCI(A/G)(A/G)(G/C)I(A/C)(A/G)AA(A/G)AA-3´) directed to genes encoding adenylation modules have been described by Turgay et al. (Pept. Res. 7, 238-241 [1994]). PCR reaction mixtures with a final volume of 25 µl contained 0.1 µg template DNA, 0.2 U Taq DNA-polymerase (Gibco BRL, Eggenstein, Germany), 5 µmol dNTP, 5% dimethyl sulfoxide (Sigma), 1.5 mM $MgCl_2$, 25 pmol of each primer and the appropriate reaction buffer supplied by Gibco BRL. Chromosomal DNA of *S. cellulosum* was used as template. Additionally, chromosomal DNA of *Myxococcus fulvus* was used with PS primers. Reactions were carried out in an Eppendorf Mastercyler Gradient (Eppendorf, Germany) using the following conditions: denaturation 30 s at 97°C, annealing 30 s at 55°C, extension 60 s at 72°C for a total of 30 cycles. The formation of ca. 700 bp fragments using the KS primers and of ca. 350 bp fragments with the PS primers were confirmed by 0.8% agarose gel electrophoresis. Fragments of independent PCR reactions were ligated into vector pCR2.1TOPO using the TOPO TA Cloning kit (Invitrogen, Leek, The Netherlands) according to the manufacturer´s protocol and transformed into *E. coli* XL1-Blue. Sequencing of the resulting plasmids and analysis of the deduced amino acid sequence revealed three different KS fragments, designated pM008.4, pM008.6, pM008.7, one PS fragment (pAPs1) corresponding to *S. cellulosum* and one PS fragment (pDPs1) obtained with chromosomal DNA of *M. fulvus*. The PCR fragments were re-isolated by digestion with *Eco*RI from the plasmids pM008.4, pM008.6, and pM008.7, labeled, pooled and used as gene probes in hybridization experiments as described below. The same procedure was performed with the PS fragments of pAPs1 and pDPs1.

Hybridization with PKS and PS specific DNA probes (see above) was carried out using the DIG nonradioactive labeling and detection kit (Boehringer Mannheim, Germany) and performed according to the supplier´s manual using buffer containing 50% formamide. The membranes were hybridized in plastic bags containing approx. 10 ml of hybridization solution at 39°C overnight. Unspecific binding of probes was removed by 2 wash steps with 2 x SSC, 0.1% SDS at room temperature for 20 min. and one stringent wash step with 0.5 x SSC, 0.1% SDS at 60°C for 20 min. Detection of hybridizing DNA fragments was performed with the above mentioned system according to the manufacturer´s protocol using CSPD as chemiluminescent substrate. The signals were recorded by exposure of the treated membrane to Hyperfilm ECL (Amersham Life Science, Little Chalfont, England) which was developed in appropriate time intervals.

71 signals were detected with the PKS specific gene probe. On the duplicate filters 35 signals were obtained with the PS specific gene probe of which 7 were already known from the PKS hybridization experiment. These recombinant cosmids harbored PKS- and PS-encoding genes. In order to corroborate these results PCR experiments were performed with DNA of the 7 recombinant cosmids as template and PKS (KS1Up, KSD1) and PS specific primers (TGD, LGG) generating fragments of the expected size of approx. 700 bp and 350 bp, respectively (primers and reaction conditions see above).

A comparison of the restriction fragment patterns of the DNA from the 7 recombinant cosmids carrying PKS and PS genes digested by BamHI facilitated an arrangement of the cosmids in

3 groups. They were represented by cosmids designated A2 and A5. The remaining group was represented by pEPOcos6. Therefore, A2 and A5 represented good candidates for further DNA sequence analysis because they carry both PKS and PS genes.

D. Random "shotgun" sequencing of recombinant cosmids and plasmids

1. Library construction

a. pEPOcos6, pEPOcos8, A5, and Sau4: pEPOcos6 and pEPOcos7 were sequenced to completion, and contiguous sequence data and analysis for these overlapping cosmids is presented below for the "cos6 region" (cf. claims 7 and 9). Sequencing of cosmid A5, pEPOcos8 and plasmid Sau4 was taken to the point of large contiguous sequences (contigs) representing the *S. cellulosum* insert; sequence and analysis presented below (cf. claims 10 to 15).

Randomly sheared libraries were constructed for cosmids and plasmids of interest using a protocol similar to that of of Fleischmann et al., 1995 (Science <u>269</u>, 496) and modified in Fraser et al., 1995 (Science <u>370</u>, 397). Briefly, Qiagen-column purified cosmid DNA (~10 μg) was sheared to a size of approximately 2 kb and the DNA end-repaired using BAL31 nuclease. The DNA was gel-purified after electrophoresis through a 0.75% low-melting temperature agarose gel containing 0.5 μg/ml ethidium bromide in 1X TAE buffer run at 80 V for 2 hours. The volume of the low-melt agarose gel slice was estimated by adding the gel slice to a microfuge tube and weighing, then 0.1 vol. of 3 M sodium acetate (pH 7) was added and the agarose incubated at 60°C. The temperature was equilibrated to 37°C, and DNA extracted twice using an equal volume of buffered phenol (Life Technologies). The aqueous phase was transferred and extracted once with an equal volume of chloroform, then ethanol precipated by the addition of 2 vol. cold 100% ethanol. DNA was concentrated by spinning at 16,000 x g in a microcentrifuge. The DNA pellet was washed with 1 ml 70% ethanol and resuspended in 100 μl of 0.1X TE. The DNA was ligated to SmaI-digested, phosphatase-treated pUC18 vector (Pharmacia), and single insert recombinants isolated by gel-purification of the band containing vector plus a single insert, followed by T4 polymerase polishing, and a final intramolecular ligation of the vector-plus-single-insert DNA. This final ligation represents a library of highly random ca. 2 kb fragments that was used for shotgun sequencing of the ca. 40 kb cosmids or ca. 10 kb plasmids.

b. Cosmid A2: Cosmid DNA with inserts of *S. cellulosum* was isolated by an alkaline lysis procedure and purified with Macherey Nagel columns (Machery und Nagel GmbH und CoKG, Düren, Germany) using manufacturer's recommendation. Purified Cosmid DNA was sonicated, end-repaired using T4 DNA Polymerase (Boehringer Mannheim, Germany). After gel-purification fragments of a size of approximately 2 kb were ligated into SmaI-digested, phosphatase-treated pTZ18R vector (Pharmacia). The ligation represents a library of highly random ca. 2 kb fragments that was used for shotgun sequencing of the ca. 40 kb cosmid.

2. Sequencing and assembly

a. pEPOcos6, pEPOcos8, Sau4, and A5: DNA (1 μl of 100 μl total in the library) was transformed into *E. coli* by electroporation (20 μl of Electromax DH10B cells from Life Technologies) and cells spread onto LB plates containing 50 μg/ml ampicillin. After growth overnight at 37 °C, transformants (ca. 300-3000 CFU total) were tranfered to 96-well growth blocks and shaken overnight at 37°C in 1.3 ml LB medium with 50 μg/ml ampicillin. Templates were prepared from these cells by an alkaline lysis procedure (Qiagen QiaQuick Turbo Prep) to yield purified, double-stranded plasmid DNA. Cycle-sequencing of the plasmid templates was performed using universal forward and reverse primers and BigDye Terminator sequencing kits (Applied Biosystems), using the manufacturer's recommendations, then resolved using an ABI377 automated sequencer. Sequences were edited using Phred, then assembled into larger contiguous sequences using Phrap (Phil Green, University of Washington, St. Louis, MO).

b. **Cosmid A2:** DNA (1 µl of 20 µl total in the ligation) was transformed into *E. coli* DH10B by electroporation and cells were spread onto LB agar medium containing 50 mg/ml ampicillin. After growth for 18 hr at 37°C, transformants were transferred to 96-well growth blocks and shaken overnight at 37°C in 1.3 ml 2x YT medium with 50 mg/ml ampicillin. Templates were prepared from these cells by an alkaline lysis procedure (Qiagen Qiaquick Turbo Prep) to yield purified, double-stranded plasmid DNA. Cycle-sequencing of the plasmid templates was performed using universal forward and reverse primers and Big Dye Terminator sequencing kits (PEBiosystems) or Thermo Sequenase fluorescent labelled primer cycle sequencing kit (Amersham Pharmacia Biotech) using the manufacturer's protocols. In the shotgun phase of a cosmid, identical amounts of samples were sequenced either by dye-primer or dye-terminator chemistries (Pharmacia, PE Biosystems). Data were collected using Licor and ABI 377 automated sequencers and assembled with the GAP4 program (Bonfield, Smith, Staden, Nucl. Acids Res. 23, 4992-4999 [1995]). Gaps were closed using custom made primers (MWG-Biotech) on plasmid templates or PCR products in combination with dye-terminators.

E. Bioinformatic Methods

1. Open reading frame (ORF) identification

ORFs were identified in the pEPOcos6 region using the OMIGA 1.1.2 (GCG 0.4D) program from Oxford Molecular Limited. Default values were used (Standard genetic code, all ORFs over 50 bases) to generate ORFs; analysis of these results lead to the list of 14 highest quality ORFs as defined in claim 9. Other ORFs, genes, or genetic elements may be found in the pEPOcos6 insert that have not yet been annotated. In addition to hand-editing of the OMIGA-generated data, the MAGPIE automated genome analysis tool:

(http://genomes.rockefeller.edu/magpie/magpie.html)

was used to identify genes for all the sequenced cosmids and plasmids. ORFs identified in this manner are presented as both nucleotide and peptide files below.

For cosmids A2 and A5, ORFs have been identified within the DNA sequences of A5 (contigs 10, 11, 12) and of A2 using the FramePlot analysis program from Ishikawa and Hotta (FEMS Microbiol. Lett., 174, 251-253 [1999] public available under [http://www.nih.go.jp/~jun/cgi-bin/frameplot.pl] which is based on positional base preference in codons typical for organisms having genomes with a high G + C content (Bibb et al., Gene 30, 157-166 [1984]). Default parameters using ATG and GTG as start codons were used. The deduced amino acid sequence of predicted ORFs were compared with protein databases (GenBank, CDS translations, PDB, SwissProt, PIR, PRF) using BLASTP (Altschul et al., Nucleic Acids Res., 25, 3389-3402 [1997]). Additionally, high scoring amino acid sequences were analyzed using the Pfam program [http://www.sanger.ac.uk/Software/Pfam/], which identified specific domain structures of the submitted proteins (Bateman et al. Nucleic Acids Res., 27, 260-262 [1999]).

2. BLAST searches

BLASTP2 similarity searches were performed using the peptide files from the above ORF identification strategy as query sequences. Searches were performed using the in-house Bioinformatics BLASTP2 (Version: BLASTP 2.0a19MP-WashU) web page at the Bristol-Myers Squibb Pharmaceutical Research Institute (allows BlastN2, BlastP2, BlastX2, TblastN, and TBlastX searches). In addition, peptide files generated by the MAGPIE analysis were automatically searched using a FASTA algorithm.

3. Best match and probable identification

Analysis of the BLASTP2 and FASTA output led to an assignment of a best match and probable function. The best match was usually the top scoring match, although sometimes another match was given because it was a more relevant homolog, or no match was found with a significance greater than >e-4. Probable function represents the best estimate of function given the initial analysis of the BLAST data and the published literature regarding the best match, and may not necessarily represent the true function of the gene product (hypothetical proteins are of unknown function). A higher probability score indicates a higher liklihood that the probable function corresponds to that of the best match; e.g., the polyketide synthase matches are all above e-100, and given the very high significance scores are presumed to function as polyketide synthases (as are the high scoring peptide synthetases).

The following is a summary of the sequence data from the pEPOcos6 region, pEPOcos8, A5, Sau4 and A2.

a. Data from pEPOcos6 region:

Summary: A large PKS/PS cluster spanning multiple cosmids. An IS element (designated IS-Sc1 here) is found in the cluster - this may be a potential tool for genetic analysis of *Sorangium*.

Statistics: Sequence was assembled from over 2000 random sequences (forward and reverse reads of the ca. 2 kb cloned fragments derived).

47,713 nucleotides of contiguous sequence (no pFD666 vector included)

DNA sequence data are as defined in claim 7.

Note: pEPOcos6_ORF7 sequences (cf. claim 9): the predicted N-terminus of ORF7 shows 145 nucleotide overlap with ORF6.

Note: pEPOcos6_ORF8 sequences (cf. claim 9): >pEPOcos6_ORF8.seq ("ORF9_up" in Fig.2)

67.3% G+C

Table 3 shows ORF data summary. Note: pEPOcos6_ORF1.seq is truncated at its 5' end; correspondingly pEPOcos6_ORF1.pep is truncated at its N-terminus.

b. Data from pEPOcos8 region:

Summary: Two PKS genes found on a cosmid. A Tn1000 insertion is also found (occurred during *E. coli* propagation). No peptide synthetase genes were found; one P450 hydroxylase was identified.

Statistics: 1952 random sequence reads from the pEPOcos8 library were assembled using phrap, with 1024 of the sequences assembling into 57 contigs. 12 of these contigs were chosen (totaling 56,537 bp) which each contained >6 reads and consisted of about 1000 bp or more. The sequences of these 12 contigs and the associated ORFs are given below.

DNA sequence data from contigs are as definded in claim 10. Table 4 shows more data.

pEPOcos8 protein data are as defined in claim 11, i.e. for selected ORFs (polyketide synthase, peptide synthetases, or ORFs with high similarity to known genes).

c. Data from cosmid A5 insert:

Summary: A cluster of PKS and PS genes found on the cosmid. Other genes possibly involved in this secondary metabolite production include a downstream lipoxygenase gene higly similar to eukaryotic orthologs.

Statistics: 880 random sequence reads from the A5 library were assembled using phrap, with 530 of the sequences assembling into 12 contigs. 3 of these contigs were chosen (totaling 41,556 bp) which each contained >100 reads and consisted of about 9000 bp or more. The sequences of these 3 contigs and the associated ORFs are given below.

DNA sequence data from contigs are as defined in claim 12. Table 5 shows more data.

Protein sequence data from selected A5 ORFs are as defined in claim 13.

d. Data from plasmid Sau4 insert:

Summary: Insert contains PKS genes on two large contigs - most similar to the soraphen PKS gene from Sorangium.

Statistics: 565 random sequence reads from the Sau4 library were assembled using phrap, with 84 of the sequences assembling into 18 contigs. 2 of these contigs were chosen (totaling 6596 bp) which each contained >10 reads and consisted of about 1000 bp or more. The sequences of these 2 contigs and the associated ORFs are given below.

DNA sequence data from plasmid Sau4 contigs are as defined in claim 14. Table 6 shows more data.

Protein sequence data from selected plasmid Sau4 ORFs are as defined in claim 15.

e. Data from cosmid A2

Table 7 shows ORF data summary

F. Construction of suitable recombinant expression vectors

1. Expression in Myxobacteria

Heterologous expression of the ORFs shown in Figure 1 is performed by using a derivative of plasmid pSUP102 (Simon, R., Priefer, U., Pühler, A., Methods in Enzymology (1986), vol. 118, pp. 643-659). In this plasmid the gene for chloramphenicol resistance is changed for a cassette comprising the gene for streptomycin resistance and the promoter element of the Tn5 transposon. Short homologous genomic DNA segments from the host organism are ligated with the DNA sequences of Figure 1 and with efficient regulatory elements into, for example, the EcoRI restriction site of the vector. Following amplifiction of the vectors in *Escherichia coli* the DNA is transfered by electroporation of the host cells or by conjugation with *Escherichia coli* S17-I (Simon, R., Priefer, U., Pühler, A., Biotechnology (1983), vol. 1, pp. 784-791).

By means of the tetracycline or streptomycin resistance, respectively, mediated by the vector the host cells are checked for integration of recombinant plasmid DNA into the chromosome by homologous recombination.

2. Expression in Streptomyces cells

Heterologous expression of the ORFs shown in Figure 1 is performed by using bifunctional Strepomyces-Escherichia coli cosmids pKU206 and pOJ466.

3. Expression in Escherichia coli cells

Heterologous expression of the ORFs shown in Figure 1 is performed by using "bacterial artificial chromosomes", cosmids (for example Supercos, Stratagene GmbH, Heidelberg) and T7 expression systems (Stratagene GmbH, Heidelberg; New England Biolabs Schwalbach, FRG). Expression of recombinant enzymes occurs in Escherichia coli cells constitutively expressing phosphopantetheinyl transferase required for the formation of holoenzyme polyketide synthetases and polypeptide synthetases.

Table 3. pEPOcos6 region gene annotation summary (continued).

GENE	5'	3'	# BP	#AA	MW (DA)	BEST MATCH (SCORE)	PROBABLE IDENTIFICATION
ORF1	1 [a]	731	732 [b]	244	26218	ACDA_BACSU (e-22)	acyl-CoA dehydrogenase
ORF2	731	2275	1545	515	56317	AF047828 (e-94)	peptide synthetase
ORF3	2301	3356	1058	352	39092	U57065 ZmaR (e-29)	antibiotic resistance gene
ORF4	3412	4050	639	213	24819	(no match)	hypothetical protein
ORF5	4248	12101	7854	2618	283282	PKSK_BACSU (e-190)	polyketide synthase
ORF6	12097	14322	2226	742	80545	Z83857 ppsE (e-111)	polyketide synthase
ORF7	14178 [c]	16451	2274	758	82007	(no match)	hypothetical protein
ORF7.1 [d]	15866	14196	1671	557	61320	Y4HP_RHISN (e-28)	hypothetical protein
ORF7.2 [d]	16507	16154	354	118	13102	Y4HO_RHISN (e-13)	hypothetical protein
ORF7.3 [d]	16815	16507	309	103	11079	Y4RG_RHISN (e-13)	hypothetical protein
ORF8	16830	17630	801	123	29633	PKSL_BACSU (e-2)	polyketide synthase
ORF9	17628	25244	7617	2539	279286	pir|S73015 (e-160)	polyketide synthase
ORF10	25235	27877	2643	881	97101	AF047828 (e-111)	peptide synthetase
ORF11	27867	32498	4632	1544	165084	AF091251 (e-167)	polyketide synthase
ORF12	32498	39922	7425	2475	267116	AF040570 (e-223)	polyketide synthase
ORF13	40031	45559	5529	1843	71258	AF091251 (e-119)	polyketide synthase
ORF13.1	45599	46018	420	140	14590	(no match)	hypothetical protein
ORF14	46015	47577	1563	521	55671	PKN1_MYXXA (e-34)	Serine/Threonine-Protein kinase

[a] The predicted ORF1 gene and gene product is truncated due to cloning of the DNA into the cosmid vector.

[b] 731 is the last nucleotide of the last amino-acid-encoding codon; 732-735

is TGA (termination codon). Termination codons have been excluded in the present annotation.

[c] note: the predicted N-terminus of ORF7 shows 145 nucleotide overlap with ORF6

[d] note: ORFs on opposite strand - make up a transposable element from bp 16863-14130 (2733 bp, 11 bp terminal inverted repeat) that is similar to IS1131 from *Agrobacterium tumefaciens* (IS-66 like element, 2773 bp, 4 ORFs, 11 bp inverted repeat)

Table 4. pEPOcos8 assembly analysis summary (continued).

a. pEPOcos8 assemblies

ASSEMBLY	SIZE(BP)
Contig43	1017
Contig44	1246
Contig48	978
Contig49	1969
Contig50	2877
Contig51	2319
Contig52	1883
Contig53	4871
Contig54	7257
Contig55	5021
Contig56	10945
Contig57	16154

b. selected ORFs from Contig 56 and 57 of pEPOcos8

gene	5'	3'	# bp	#aa	best match [score]	probable identification
Contig56_003	3	8675	8673	2890	ERY2_SACER (e-300+)	polyketide synthase
Contig56_027	10784	8682	2103	700	pir|I60218 (e-300+)	transposon Tn1000 (*E. coli*)
Contig57_001	92	1210	1119	372		
Contig57_002	222	7001	6780	2259	AL021899 pks12 (e-267)	polyketide synthase (M. tuberculosis)

Contig57_026	7424	6975	450	149		
Contig57_027	7116	8375	1260	419	CPXK_SACER [e-50]	Cytochrome P450 monooxygenase
Contig57_030	9074	8337	738	245		
Contig57_031	8412	9080	669	222		
Contig57_032	8432	9667	1236	411		
Contig57_033	9724	8600	1125	374		
Contig57_037	10621	9755	867	288		
Contig57_039	11085	10618	468	155		
Contig57_040	10687	11091	405	134		
Contig57_041	11887	10904	984	327		
Contig57_043	11520	12998	1479	492	AF072709 [e-42]	unknown ORF (S. lividans)
Contig57_044	13730	12018	1713	570		
Contig57_047	13093	13797	705	234		
Contig57_048	14064	13138	927	308		
Contig57_049	14371	13535	837	278		
Contig57_051	13900	14394	495	164		
Contig57_052	14036	14440	405	134		
Contig57_053	14678	15715	1038	345		
Contig57_056	15211	15900	690	229		

Table: 5. A5 assembly analysis summary (continued)
a. pEPOcos8 assemblies

contig	bp	ORF	5'	3'	bp	G+C content pos.3	best match [score]	probable function	identified domains using Pfam
10	9435	1	2861	582	2280	88.6 %	AAC44128 (e-170]	peptide synthelase [Saframycin]	AMP-binding aa 68-512; pp-binding aa 631-697
		2	3525	2902	624	87.0 %	no match		
		3	6420	4195	2226	95.1 %	P38370 [3e-04]	OmpA like	
		4	7734	7135	600	98.0 %	P39760 [2e-21]	unknown	
		5	9434	7950	>1495	96.2 %	no match		
11	18023	1	2526	751	1776	97.1 %	CAB38518 [e-134]	peptide synthetase	AMP-binding aa 118-520;
		2	3586	2501	1086	94.5 %	CAB38516 [e-12]	peptide synthetase	DUF4 (domain of unknown function, found to the carboxy side of pp-pinding sites) aa 5-360;
		3	5210	3579	1632	97.8 %	S53999 [e-102]	peptide synthetase [Pyoverdine]	pp-binding aa 1-30; DUF4 aa 51-442; conflict. ca. 20 aa at N-terminus are missing (conserved serine residue)
		4!	6261	3811	2649	64.4 %!!	CAA11039 [7e-55]	polyketide synthase [Rifamycin]	conflict!!
		5	8087	6258	1830	94.8 %	CAB06094 [e-144]	polyketide synthase (Phenolpthiocerol Mycob.)	ketoacyl-synthase aa 14-439;
		6	17320	8090	9231	92.8 %	AAD04757 [e-180]	peptide synthetase [Lichenysin]	AMP-binding aa 371-758; pp-binding aa 840-904; DUF4 aa 937-1319; AMP-binding aa 1438-1825; pp-binding aa 1907-1071; DUF4 aa 1999-2388; AMP-binding aa 2485-2889; pp-binding aa 2972-3004; pp-binding aa 3027-3046;
12	15898	1	1	1545	>1545	97.5 %	AAC68816 [4e-74]	peptide synthetase (FK506]	DUF4 aa 45-426;
		2	2883	1549	1335	94.4 %	P43492 [e-07]	cytochrome P450 enzyme	
		3	4659	2911	1749	92.5 %	NP 001130 [5e-56]	lipoxygenase	
		4	5896	7086	1191	95.2 %	no match		
		5	7094	7822	729	90.1 %	no match		
		6	8974	7943	1032	87.8 %	no match		
		7	12001	11252	750	92.8 %	no match		
		8	13533	12181	1353	93.3 %	no match		
		9	15897	13981	>1917	93.9 %	CAA19149 [e-09]	regulator	
	43356								

Table 5.

b. selected ORFs from cosmid A5

gene	5'	3'	# bp	#aa	best match [score]	probable identification
Contig10_001	2861	582	2280	759	U24657 saframycin (e-155)	polyketide synthase
Contig10_006	2880	3323	444	147		
Contig10_007	3876	2902	975	324		
Contig10_008	2953	3957	1005	334		
Contig10_009	4357	3299	1059	352		
Contig10_013	4180	6585	2406	801		
Contig10_016	7033	5600	1434	477		
Contig10_017	7043	6138	906	301		
Contig10_018	6500	7219	720	239		
Contig10_019	6954	7295	342	113		
Contig10_020	6982	7797	816	271		
Contig10_021	7819	7040	780	259		
Contig10_023	7415	8029	615	204		
Contig10_024	7794	9435	1642	548		
Contig10_027	9435	8806	630	209		
Contig11_001	770	417	354	117		
Contig11_002	2526	751	1776	591	AL035640 (e-113)	peptide synthetase
Contig11_004	1033	2787	1755	584		
Contig11_005	3500	1977	1524	507		
Contig11_007	3586	2501	1086	361		
Contig11_008	2507	3814	1308	435		
Contig11_011	5213	3579	1635	544	AF047828 syringomycin (e-86)	peptide synthetase

Contig11_012	6459	3811	2649	882	AJ223012 (e-52) rifamycin	polyketide synthase
Contig11_016	6511	5210	1302	433		
Contig11_018	5551	6735	1185	394		
Contig11_021	9899	6258	3642	1213	Z83857 ppsE M. tuberc (e-129)	polyketide synthase
Contig11_026	17329	8090	9240	3079	AF047828 syringomycin (e-300+)	peptide synthetase
Contig11_048	16733	17365	633	210		
Contig11_049	17397	17723	327	108		
Contig12_001	1	1545	1545	514	AF082100 (e-63) (Streptomyces)	peptide synthetase
Contig12_002	1368	1	1368	456		
Contig12_003	3	1655	1653	550		
Contig12_005	2317	1361	957	318		
Contig12_006	2883	1549	1335	444		
Contig12_007	1777	4926	3150	1049		
Contig12_009	4659	2911	1749	582	LOX5_MOUSE (e-54)	ARACHIDONATE 5-LIPOXYGENASE
Contig12_011	4523	5065	543	180		
Contig12_012	4638	5231	594	197		
Contig12_013	4942	5520	579	192		
Contig12_014	6056	5541	516	171		
Contig12_015	5765	6373	609	202		
Contig12_016	5896	7086	1191	396		
Contig12_017	7095	5899	1197	398		
Contig12_018	5955	7331	1377	458		
Contig12_020	7549	7010	540	179		
Contig12_021	7094	7822	729	242		
Contig12_022	7995	7318	678	225		
Contig12_023	8408	7716	693	230		
Contig12_024	7916	9550	1635	544		

Contig12_029	10751	9732	1020	339
Contig12_030	9795	11132	1338	445
Contig12_033	10880	12124	1245	414
Contig12_035	12184	11252	933	310
Contig12_036	12079	14098	2020	674
Contig12_039	14098	12248	1851	616

Table 6. Sau4 assembly analysis summary.

a. plasmid Sau4 assemblies

Assembly	size(bp)
Contig17	2581
Contig18	4015

b. selected ORFs from cosmid A5

gene	5'	3'	# bp	# aa	best match [score]	probable identification
Contig17_001	2485	1	2485	829	U24241 *Sorangium* [e-213]	polyketide synthase
Contig18_002	2	1510	1509	502	U24241 *Sorangium* [e-105]	polyketide synthase
Contig18_010	1494	4015	2522	841	U24241 *Sorangium* [e-245]	polyketide synthase

Table: 7. ORF data summary from A2 insert

ORF	5´	3´	bp	G +C content pos.3	best match [score]	probable function	identified domains using Pfam
1	1666	1	>1666	94.4 %	P54744 [5e-37]	regulation [serine/threonine protein kinase]	pkinase aa 47-294:
2	1605	3338	1734	90.7 %	no match		
3	6100	3398	2703	98.0 %	CAA15124 [>e-180]	acyl-tRNA synthetase	tRNA-synthase aa 27-694;
4	7111	6374	738	94.7 %	AAC32457 [2e-17]	monooxygenase	oxidoreductase FAD/NAD-binding domain aa 110-227;
5	9590	8433	1158	74.4 %	CAB42045 [9e-67]	aminotransferase	aminotran_1 aa 2-385;
6	11393	9855	1539	85.5 %	AAD21754 [e-113]	L-dopa decarboxylase	pyridoxal deC aa 46-411
7	13656	12712	945	86%	CAB41201[7e-41)	oxidoreductase	short chain dehydrogenase domain aa 53-240;
8	15374	19984	4611	87.6 %	CAB06094 [<e-180]	polyketide synthase	ketoacyl-synthase aa 13-438; acyl transfase aa 533-854; short chain dehydrogenase domain aa 1159-1357; pp binding aa 1451-1515;
9	20003	27889	7887	88.0 %	AAC80285 [<e-180]	polypeptide synthetase	DUF4 aa 17-409; AMP-binding aa 507-905; pp-binding aa 991-1054; DUF4 aa 1067-1466; DUF4 aa 1544-1944; AMP-binding aa 2041-2439; pp-binding aa 2525-2589;
10	28251	29402	1020	86.6 %	BAA13079 [2e-44]	peptidase	
11	31720	30401	1320	98.9 %	no match		
12	31982	32932	951	95.3 %	CAB09733 [2e-63]	sigma factor	Sigma70 ECF aa 17-83;
13	33128	33613	486	95.7 %	no match		
14	33661	34077	417	94.2 %	CAA19900 [e-37]	regulation	
15	35611	35255	357	80.8 %	CAA19859 [3e-15]	regulation	HTH aa 5 11-109;
16	37856	35730	>2127	96.8 %	BAA17885 [2e-50]	regluation	response reg aa 46-159; signal aa 326-542; response reg aa 590-703;

Claims

Claims

1. DNA sequence, the expression products of which cause an enzymatic biosynthesis, a mutasynthesis or a partial synthesis of polyketide or heteropolyketide compounds or are involved therein.

2. DNA sequence according to claim 1, wherein the polyketide or heteropolyketide compounds are epothilones.

3. DNA sequence according to any of the preceding claims, wherein the DNA is derived from myxobacteria.

4. DNA sequence according to any of the preceding claims, wherein the DNA is derived from Sorangium strains.

5. DNA sequence according to any of the preceding claims, wherein the DNA is derived from Sorangium cellulosum.

6. DNA sequence according to any of the preceding claims, wherein the DNA is selected from the group consisting of:

(a) the following DNA sequence:

Seq ID No 1 (A2 cosmid)

GGATCGCGGCGCCCTCGCGCTGCTCCTCGAGCGTGCGGAGGAACTCCCACGCCAGGCGCGACT
TGCCGAGGCCAGGCGCGCCCACCACCACCACCGCGTTCGCGGAGGGCTCGTCGACGCAATGGC
GCCACTCGGTCGCGAGCTGCGAGAGCTCGCGCTCCCGCCCCACGCAGGGCGTCGGCTTGCCGA
GGAGCCGTGGGACGGCATCCGGCTCCTCCTTCGGGCCGCGAAGCCAGCACCCTCCGGGCCCCT

GTACCGTCTCGAAGCGGCTCGCGAGCAGGCTGGCCGTCGCGTCGTCGAGCCGGATCTCCGGCG
GCGACAGGCCATCTCGCCCGGCGATGAGCTGCGCGACCCGATCGACCAGCTCGCCGACCGGCA
GCCTCGCCTCGACCTCGGCCAGCCCTGTCGCGACGGACACGGGCACGCCTCCGAGCGCCGCCC
GCAGCGCGAGGGCGCAGTGGGCCGCCCGTGTGGCGAGATCCGTGGGCGACTCGGCGCCGGACA
GCGCGACGAGCCACCAGCGCGCTTGCAGCCGATCGAGGCGCCCGCCGTGGCGCGCCGCGATGT
CCCGCAGCGCCTCGGCCCGCGCGGCGCCGTCGTCCTCCGAGAGCGTGGCGCCGGCCTCGGCGC
CGCCGTCTTCGGCCAGGATGACGCACATCACCTTGCGCTCGGCCGTCGTGATCGCCTCGCCCG
GCGCGGCCGGCGCCGCGACCGCGCTCGCCCCGATCGAGAGCCCCTCGCCGGCCACGGCGGCGA
GCTCCGCCGCGGCGGCGGCGCCGTCGCGCGGCCGCTCTCCCGCGTTCTTCGCCAGCATCCGCG
CCACCAGGCGCTCGAGCGGCTCCGGGATACCGTCGCGGAGCTCCCCGAGCCGCGGCGGCTCTT
CCAGGACGACCCGCATCAGGAGCGCGAGCGCGCTGTTGCCGAGGAACGGCGGGCGCCCCGCGA
GGCACTGGAACAGCACGCACCCGAGCGCGAACACGTCGGCCCGGGCGTCGACCGGCGCGTCGC
CGCGCACCTGCTCGGGCGCTATGTACCCGGGCGTGCCGAGCACGGCCCCGGGCGACGTGAGGG
TCGGCGCGAGCCGGAGGTGGCGCGCGATGCCGAAGTCGAGCAGCGTGACGCGCTCGACCGCGC
CGCCCACGAGCATCAGGTTGCTCGGCTTGAGGTCGCGGTGAACGACGCCGAGCCAGTGGATCG
CGCCGAGCGTCGTGGCCACGCGCGCGGCCAGCGCCACGCTCTCGGCCAGCGTGAGCGGCGCCC
CGGCGAGCCGCTCCTCCAGGGTCACGCCGTCGAGCCACTCCATGGCCAGGTACGGCCGCCCTG
CGCCGGTCACCCCGTGCGCCACGTACTGCACCACGCCGGGCAGCCGGAGCGTCACGAGCGCCT
CCGCCTCCCGCGCGAACCGGCGCAGGTCGTTGGCGCTCGCGCCCTGCAAGACCTTGAGCGCGA
CCGCCTGCCCGGACACCCGGTCGCGCGCCCGGTACACGTCCCCCATCCCGCCGGAGACGGCGA
GCCGCTCGATCTCGAAACGATCCTCGATCACATCCGCTGCGCGCATGGCGGTGCCAATGTACT
CCGCGCGAGCCTCGGGCCCCCGCGCGTAAGTGCGGCCCTGCGCCCGGTTGAACGCCAGCCCGA
GCGTGACCGCCTCGCGCTCGGGATCCACGGCCGCCGGATCGGTCCACGCCTCGACGAGCGCCT
GCGTTGAACAACCCGCCACCGGGCGCACGCAGCCGGCATCGCCGCGCTGGCCACCCGGCGCTG
CCGCCCTTAGGCTCACCTCCGCGATGCCCCGCTGGTTCAACACGGCAGGTCCCTGCAACCCGG
CCGATCACTACATGCTCCCGGCCGAGGAGCGCTTGCCCGCAGTGCGCGATCTGGTCGATCGCA
AGGCCTACTTCGTCCTGCACGCCCCGCGGCAGATCGGCAAGACGACCTCGCTGCGCACGCTCG
CCCAGGATCTCACGGCCGAAGGGCGCTACGTGGCCGTCCTCGTCTCGGCGGAGGTCGGCGCCC
CCTTCTCTGACGATCCCGGCGCGGCCGAGCTCGCGATGCTCGCAGAATGGCGCGGCACCGCCG
GCGCGCAGCTCCCCGCCGATCTGCGGCCGCCACCGTTCCCCGATGCGCCCGCCGGTCAGCGCA

TCGGGGCCGCCCTGCGCGCCTGGGCTCAGGCCGCGCCGCGCCCGCTCGTCGTCTTCCTCGACG
AGGCCGACGCCCTGCGCGACGCGACGCTCGTCTCCCTATTGCGCCAGATCCGCAGCGGCTATC
CCGACCGCCCGCGTGACTTCCCGCACGCGCTCGCCCTCGTCGGCCTGCGCGACGTGCGCGACT
ACAAGGTCGCGTCGGTCGACAGCGGCAGGCTCGGGACGTCGAGCCCCTTCAACATCAAGGTCG
AGTCGCTCACGCTGCGCAACTTCACCCGCGACGAGGTCGCAACACTCTACGCTCAGCACACGG
CCGAGACCGGTCAGGTCTTCCGGCCGGACGCCGTGGACCGCGCCTTCGAGCTCACCCAGGGCC
AGCCGTGGCTCGCCAACGCGCTCGCCCGCCAGCTCGTCGAGGTCCTCGTCAAGGACCGCGCGC
AACCCATCACGTCTGCGAACGTCGATCGCGCCAAGGAAATCCTCATCGAGCGGCAGGACACAC
ACCTCGACAGCCTGGTGGATCGGCTGCGCGAGCCGCGCATCCGCGCGGTGATCGAGCCGATGC
TCGCCGGCACCGCGTTGCCGAGCGTGCCCCCCGACGACCTTCGTTTCGCGATCGACCTCGGCC
TCGTGCGCATGACCGCGGAGGGCGGCCTCGACGTCGCCAACCCCATCTACCGCGAGATCATCG
TCCGCGAGCTCGCGTTCCCGATCCGCGCCTCACTCCCCCAGATCAAGGCCACGTGGCTCACGC
AGGACGGCCGCCTCGACGCGGACCGCCTGCTCGACGCCTTCCTCTCCTTCTGGCGCCAGCACG
GCGAGCCGCTCCTCGGCGCCGCGCCCTACCATGAGATCGCCCCGCACCTCGTGGTGATGGCCT
TCCTCCACCGCGTGGTGAACGGCGGTGGCACCGTCGAGCGCGAGTACGCCATCGGCCGGGGCA
GGATGGATCTCTGCGTTCGTTACGCGGGCGAGACGCTCGCGATCGAGCTCAAGGTCTGGCGAG
ACGGCCGCCCCGATCCCGTCGCCGAGGGGCTCGCCCAGCTCGACGAGTACCTGGCCGGCCTGG
GCCTCGATCGCGGATGGCTCATCCTCTTCGACCAGCGCTCCGGACAGCCCCCCATCGCCGAGC
GCACGCGCCGCGAGCGCGCGCTCTCCCCCGCCGGCCGCGAGGTCGCCGTCATTCGCGCCTGAG
GGAGCTCGCCGCGCGGCGAGCGCCCTCCACGAGGGCCGGGCCACCTCGGACAGCGTCTCTACT
CCTCCGAGGCCGCCGCGCCCCCCGCCCCGGCCGCCGCCGCCGCCGGCTCCAGCTCGCAGC
GCACCACCAGGACCTCGCCATCCGCGAGCTCCGGCCGCTCCACGAGCGCGTGCGCGCCCGCGC
GCACCGCCGTGAGCACGTCTCCCAGCGCCGGCTTCAGCCGCGCCAGCGTCGCGGCGTTCGCCC
CGAGCGCGAGGTCGGTCACGACGCGCCCCACGCTCGCGCCGAGCTCGCTCTTGCGCTTGTTGA
CCGCCGCCATCGCCGCCGCCGCCAGATCCAGGAGCCCCGGATCCGAAGGCGCCGCGACCGCCG
CGAAATCCGCCGCTGAAGGCCACTTCGCCCGGTGGATCGAGGTATCGCCCGTCTCCTCCGCGT
ACACCCAGCGCCAGACCTCGTCGGTGATGTACGGCAGGACCGGCGCGAACAGCCGCAGCAGCA
CCGACAGCCCGAGCCGCAGCGCCGCCACCGCCGAGCCGCGCGCCGCCTCCCCGGCGCCGCCCT
CGCCGCGCGCCCGCGCCTTCGCGAGCTCCAGGTAGGCGTCGGTGAACCAGCGCCAGAAGAAAT
CCTCGGTCCGCTCGAGCGCCGCCGCCGAACTCGTGCTCGTCGAACGAGCGCGTCGCGTCGTCCA

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CCACGGCCGACAGCTTGTGCAAGAGCGCCCGGTCGAGCTCCTCGGAGATCGGGTGGACCTCCG
CCGACTGGCTGAGCACGTACTTGCTCGCGTTCCAGATCTTCGTGACGAGCCGCTTGCCGATCT
TCAGCACCTTCTCGTCGAACGCCGTGTCCGTGCCGAGCCGCGCGCTCGCCGACCAGTAGCGGA
CCGCGTCCGAAGAATACGTGTCGAGCAGGTGCATCGGCGTGACGACGTTGCCCTTGCTCTTCG
ACATCTTCTTGCGATCCGGATCGAGGATCCACCCGGAGATCGCGACGTGGTGCCACGGGACCG
ACGACTCGTGCAGCATCGCCTTCGCGATCGTGTAGAACGCCCACGTCCTGATGATGTCGTGGG
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GGCCCCTCGCCCGCCGGCCGGGACGCCGGCGCCTGCTCGCCGCGGAGCCACTGCGCGGCCTCG
TCGAGGAAGGGCGCGGCGTCCCGCCCCCCCGCGGCCGGCGCCGAGGCCGGCGCGAC

or its complementary strand,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA-sequences according to (a) encoding proteins or to fragments of said DNA-sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products.

7. DNA sequence according to claims 1 to 5, wherein the DNA is selected from the group consisting of

(a) the following DNA Sequence:

Seq ID No 2 (>pEPOcos6 region)

GGATCACCTGCGGCGCGATCGCCGACCTCGTGCTGGTGTTCGGCTCGCTGGATGAGAAGCCGG
CGGCGCTACTGATAGAGACGGCGACGCCCGGGCTGCGGGTGGAGCGGTTGCGGGAGATGCTCG
GCTTTCGGGCGGCCCACCTGGCGAAGCTGTCCTTCGACGGTTGCGAGGTCCCCGAGGCTCAGC
TGATTGGCCGGCCCGGCTTTGCGCTGATGTATCTGGCCCCCTACGCCCTGGATTTCGGTCGGG
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CCAACCTGGGGATTCACCACCAGGCGACGCTGCTCCACACGCTGCAGGCCTGCCGCGCCAGGG
ATCGCGGCGACGTGACCGCCTCCGAGGCCACCCTCGCCGCCAAATACCTCGCGTCGCGGACGG
CGGTCCAGGAGACGACCAACGCGGTCCAGATCATGGGCGCGCTGGGCTGCGACGAGGAGGGCG
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GATTATCGCACTTGAATTCGCG

or its complementary strand,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA-sequences according to (a) encoding proteins or to fragments of said DNA-sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products.

8. DNA sequence according to claim 6 selected from the following

(a) open reading frames:

	Nucleotide Position	
ORF1	1666 - 1	Seq ID No 3
ORF2	1605 - 3338	Seq ID No 4
ORF3	6100 - 3398	Seq ID No 5
ORF4	7110 - 6374	Seq ID No 6
ORF5	9590 - 8433	Seq ID No 7
ORF6	11393 - 9855	Seq ID No 8
ORF7	13656 - 12712	Seq ID No 9
ORF8	15374 - 18984	Seq ID No 10
ORF9	20003 - 27889	Seq ID No 11
ORF10	28251 - 29402	Seq ID No 12
ORF11	31720 - 30401	Seq ID No 13

ORF12	31982	-	32932	Seq ID No 14
ORF13	33128	-	33613	Seq ID No 15
ORF14	33661	-	34007	Seq ID No 16
ORF15	35611	-	35255	Seq ID No 17
ORF16	37856	-	35730	Seq ID No 18

or DNA sequences complementary to said open reading frames,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA sequences according to (a) encoding proteins or to fragments of said DNA sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products,

and peptide sequences corresponding to said open reading frames

SEQ ID No 19 (>ORF1)

VDPEREAVTLGLAFNRAQGRTYARGPEARAEYIGTAMRAADVIEDRFEIERLAVSGGMGDVYR
ARDRVSGQAVALKVLQGASANDLRRFAREAEALVTLRLPGVVQYVAHGVTGAGRPYLAMEWLD
GVTLEERLAGAPLTLAESVALAARVATTLGAIHWLGVVHRDLKPSNLMLVGGAVERVTLLDFG
IARHLRLAPTLTSPGAVLGTPGYIAPEQVRGDAPVDARDVFALGCVLFQCLAGRPPFLGNSAL
ALLMRVVLEEPPRLGELRDGIPEPLERLVARMLAKNAGERPRDGAAAAAELAAVAGEGLSIGA
SAVAAPAAPGEAITTAERKVMCVILAEDGGAEAGATLSEDDGAARAEALRDIAARHGGRLDRL

QARWWLVALSGAESPTDLATRAAHCALALRAALGGVPVSVATGLAEVEARLPVGELVDRVAQL
IAGRDGLSPPEIRLDDATASLLASRFETVQGPGGCWLRGPKEEPDAVPRLLGKPTPCVGRERE
LSQLATEWRHCVDEPSANAVVVVGAPGLGKSRLAWEFLRTLEQREGAAI

SEQ ID No 20 (>ORF2)

VRPCARLNASPSVTASRSGSTAAGSVHASTSACVEQPATGRTQPASPRWPPGAAALRLTSAMP
RWFNTAGPCNPADHYMLPAEERLPAVRDLVDRKAYFVLHAPRQIGKTTSLRTLAQDLTAEGRY
VAVLVSAEVGAPFSDDPGAAELAMLAEWRGTAGAQLPADLRPPPFPDAPAGQRIGAALRAWAQ
AAPRPLVVFLDEADALRDATLVSLLRQIRSGYPDRPRDFPHALALVGLRDVRDYKVASVDSGR
LGTSSPFNIKVESLTLRNFTRDEVATLYAQHTAETGQVFRPDAVDRAFELTQGQPWLANALAR
QLVEVLVKDRAQPITSANVDRAKEILIERQDTHLDSLVDRLREPRIRAVIEPMLAGTALPSVP
PDDLRFAIDLGLVRMTAEGGLDVANPIYREIIVRELAFPIRASLPQIKATWLTQDGRLDADRL
LDAFLSFWRQHGEPLLGAAPYHEIAPHLVVMAFLHRVVNGGGTVEREYAIGRGRMDLCVRYAG
ETLAIELKVWRDGRPDPVAEGLAQLDEYLAGLGLDRGWLILFDQRSGQPPIAERTRRERALSP
AGREVAVIRA

SEQ ID No 21 (>ORF3)

VTIKKTFRSIDPATLPKHFDSPVAELRLADLWEADGTYRYDPSRPREETFVVDTPPPTASGSL
HIGHVFSYTHTDVVVRQRRMRGFNIFYPMGWDDNGLPTERRVQNYFHVRTDVRTPYERGLTLP
QAAPETIKKEPPRIVSRPNFIELCHKVTREDEQVFKALFRRVGLSVDWRNEYATIDDHCRRTA
QLSFLDLHEKGHLYSVFAPTMWDVDFQTAVAQAEVEDRPQSGAFHDIAFAVEGTAEELVIATT
RPELLAACVGVTAHPEDPRYQHLFGKTALTPIFRAPVPIFPSPLVDREKGTGILMVCTFGDAT
DVIWWREQKLPLRQMLGKNGRVLPVTFGEGAWESRDPAAANAAYAPLQGRGVKQARAAVVELL
RREEHAAAPGRGPALRGEPRPIERAVKFYERGDQPLEFVPTRQWFVRLADKKAELLEYGDKIK
WHPDFMRLRYRNWTEGLQGDWCISRQRYFGVQFPVWYPLDAEGNPDHSRPLLATREMLPVDPT
VDVPPGYEASQRDQPGGFTAESDVFDTWFTSSLTPQISSHWGDDPARHARLFPADLRPQAHDI
IRTWAFYTIAKAMLHESSVPWHHVAISGWILDPDRKKMSKSKGNVVTPMHLLDTYSSDAVRYW
SASARLGTDTAFDEKVLKIGKRLVTKIWNASKYVLSQSAEVHPISEELDRALLHKLSAVVDDA
TRSFDEHEFAAALERTEDFFWRWFTDAYLELAKARARGEGGAGEAARGSAVAALRLGLSVLLR
LFAPVLPYITDEVWRWVYAEETGDTSIHRAKWPSAADFAAVAAPSDPGLLDLAAAAMAAVNKR

KSELGASVGRVVTDLALGANAATLARLKPALGDVLTAVRAGAHALVRPELADGEVLVVRCELE
PAAAAAAGAGGAAASEE

SEQ ID No 22 (>ORF4)

MIHAEPFEARLVAARPLSPFVRELSFERADGRSFLFEAGQWVNLVLPLPGGEVKRAYSIASAP
DGSPRFDLAVTLVQGGAGSEHLHRLEPGATLRAIGPHGLFTRDPGDSAPSLFVATGTGITPLR
SMLRASLRAGLAAPHLWILFGARFEEDVIYRDELEALARGSDRIRYEITLSRGGPSWAGRRGY
VQAHVPELYRELAEKSGDPAPHVFICGLDRMVSSVRELARGELGVHRKHVHVERYD

SEQ ID No 23 (>ORF5)

MKSLPSDRAARLAQSDIRTMTLACAKVHGINMSQGVCDTPVPSVILQAVKEAMDRGCNTYSRF
DGIVELRHAIAAKLARHNGIAADPETDITVSAGATGAFQATCMALLNPGDEVLLFEPFYAYHA
QAILAVEAVPRYVTARSLSWNVDGDELERAITPKTKAIVVNSPGNPSGKVFGRMELEQIADLA
CHHDLMVITDEIYEYFIFDGREHVSVASLPRMSERTITIGGYSKTFSITGWRIGYSVADARWA
KAIGAMSDLLYVCAPTPLQHGVAAGIRGLPRSFYTGLAQGYERKRDRFCRALEKAGLPPCVPQ
GTYYVLADVSRLPGRTGRERAIYLLDETGVAGVPGDAFFEGTQGSRFMRFCFAKTDEDLEEAC
QRIEQLA

SEQ ID No 24 (>ORF6)

VSDPRKERLGDMDLEEFRRIGMRIIDWAADYLGHPDRYPVFPAIRPGDVKGRLAPTPPVEPEP
MDAVLTDFEQIILPGITHWNHPRFFAYFANTASGPGILGELLAACLNVNVMLWRTSPAATELE
ELVLSWLRQMLDLDAGLHGAIMDTASTASMVAIAAARDSAEPTIRLRGMAGQRRMRLYASEQA
HSSIEKAAITLGIGQEGVRKIPTDPAFRMVPEALRAAVVEDLGAGLRPFCVAATVGTTSTTSV
DPIPAIVSVCREHGLWLHVDAAYAGMAAIVPEHRDVLAGCEGADSLVVNPHKWLFTPMDCSVL
YVRDADRLKRAFSLVPEYLRTEGDVTNYMDWGIQLGRRFRALKLWMIVRYFGHEGLAARIREH
LRLGQQLAQWVDADPDWERLAPTPFSTVCFRMRPSALACIMRSADEAERESIERELDRLNEAL
LDEVNKSGRVFLSHTRLHGRYTIRVAIGNIRSDEVAVREAWECLRAAGARLCADERFVSCSRS
ADEGRGKS

SEQ ID No 25 (>ORF7)

MRREEPVLEAFYERYCAAPRETSYHVELPVDVELHQEAAPALPQARSLELAGRVALVTGSSRG
IGKAIALRLAEQGADVAVNYHSNKDAAEQTAAEIRALGRRTMVVQADVTRPNAAAELFSSVEA
QLGPIDILVNNVGDFFFKPLAAMTDDEWRNVMDSNLSSVHYLCRAAVARMRQRKSGRIINIGL
SPTYAIRGAPNVAAYSIAKTGVLILTRSLATEEAPHGILVNCVSPGLIDNGYLPPAQKEWMER
RVPMGRLGRASEVADAVAFLASDRASYVSGANIAVAGGWDWTDRGTEHDRRVDLFIGHEEP

SEQ ID No 26 (>ORF8)

MSGRFPGARNVEELWQKLRAGVECVVTFTEAEALAAGVSREMLANPSYVRRGAPLDGVELFDA
SFFGFSPREAESMDPQQRIFLEVAWEALERAGYDPDAHSGPIGVFAGSAPSGYHSLAQSDPEI
LGALGHYQLTLNNDKDYLTTHASYKLNLRGPSVCVQTSCSTSLVAVVMACQSLLNHECDMALA
GGVGIHAHQRRGYLYQENGISSPDGHCRAFDVAAKGTVGGSGIGIVVLKRLADALADGDHVHA
VIRGAAINNDGSSKIGYTAPSVQGQAEVIGMAQALAGVEPDDISYIEAHGTGTPLGDPIEIAA
LTRVFRAKTARRQFCAIGSLKTNLGHLDAAAGVASLIKTVMALEHRELPPSLHFERPNPKLEL
ESSPFYVNTRLTPWHAARGPRRAGVSSFGIGGTNAHVVLEEAPAPPPSGPSRRWQLLTLAARS
EAGLARATADMIEHLDRHSGTSIADVTYTSHVGRRAWPFRRAVVGESAADLRAALASEGSPRS
ISSCQAARERPVVFLFPGQGAQHLFMARELYEVEPIFRQSLDRCAELLRGPLGLDLRQVLYPA
EGQRDDAEQELGRTAIAQPALFAIELSLAKLWMAWGIVPQAMIGHSVGEFAAACLAGIFREED
ALRLVAERGRLMQQMPPGAMLAVPLAEPELAPYLSDDISLAAINGPALSVVAGPIEAIDALAA
ELLDHGLSCRRLHTRHAFHSKMMAPVVDAFTRCVSAVERRPPSGHFLSTLTGGWISPEAATIP
AYWARQLVEPVRFAQAVRQLLSESTWLWLELGPGQTLSPLVRQQARADGGQVVVASLPRAKDA
GADHLAVIEALGRVWSAGGTVDWKRFHEGEARRRVLLPTYPFERQRYWASPRHTSAPPEAIIK
PLLAKNPNVADWFFLPAWRRSDPPVSFDAQAVTTRRSTWLVFIGDEGLGAALVEGLARRGHEV
VAVVTGERFEQTGTQRYTIDPAANGDVASLFARLEIEGRMPDRIVHAFCTSPADGARIERGAA
LEIERRLGFDSLLLLAQVIAAQRHPKPLMLGVITTRAHSVIGTEIIEPLRALVLGPCRVIPQE
IPHVSCRNIDIDLPGEGGRAEIAARLIADLERESPDSVVAYRGGRRWVESIELTDVGRRSAGA
APRLRQRGAYLITGGLGGIGLVAAELLAREAHARLILVGRTGLPARQGWDDWLAAHGAGDATS
RKILRIRALEEAGAEVKIAAADVSDFNAMRSVIEEARTRFGRIDGVIHSAGIASGGMIQLRTP
MAAWRVMAPKVGGTLVLDALLRDERPDFLLICSSLASLVGGATQIDYCAANAFLDAYAQSREG
EEGCRVISVQWDTWSDVGMAVDFKLPADLQEGRRESLKRGISSSEGAEVLGRILSAGMSGPLA

ICTSDLPAYKQSVTTRRSQHEQTPAARPMHSRPTTTGAYVAPETETERRIAAIWQDLLGLEQV
GANDDFLQLGGHSLLATQVLSRVLQTLKVGISLPQFFDAPTVAGLSRLVDAARAEGAGPVAPA
IGRVERDAYRIKPPAAEQAARTKP

SEQ ID No 27 (>ORF9)

MEPVGGVDMNQPAKQQETCVFPTSFAQRRLWFLDQLEPGSAVYNMPASFRTRGPYDVDSLVRS
VNEIVRRHESLRTTVDVIDGEPVQVIAPSLRIEVPVVDLSEIDEPEREAEARRLMAEESRRPF
DLTRGPLLRAKLLRLGEADHVLILTMHHIVSDGWSMDVLFKELSTLYAAFHEGRPSPLPELPI
QYADFAVWQRELLQGEVLESHLGYWREHLRGAPTLLELPMDRPRPPAQTFRGSQRAFRLPLSL
QQAVQALSRQEGATPFMTLLTAFSVLLSRYARQSDLVVGTPIANRTRAELEGLIGFFVNMLAL
RIDLGGDPSFRELLGRVREVTLGAYAHQDLPFERLVEELSPGRSPSHSPLFQVSFTLQNTPMD
ATNRADIASGGAPLVEMKAAKFDLILELSESPQGLLGTFEYNTDLFDAGTIERMAGHLEVLLS
SAVAAPDRPIAELPLMGAEERSRVLVEWNSTAALYPEDHCMHELFEQQVERSPEATAVLLQQQ
TLTYRELNMRANQLAHHLRSLGVGPEVRVGLYLERSIETVVAILGVLKAGGAYVPLDPTYPSE
RLGLMMADAAPSVLLTQASLLSKLPPHGDATLVQLDALHEALSRLPHHTPRSGVTAQNLAYVM
YTSGSTGRPKGVLVEHRGLCNLPTVQAKLYGIAPGDRLLQFAPLCFDTSFCEIALALLSGATL
VMGTADELLPGPPLVELLKKHAVTAMLLAPTVLAALPEQQSAALPLRVLTMAGEACPAELVKR
WKAPGRRLFNSYGPTETTIWASSAADLSDERIPPIGRPIANTQIYVLDEALEPVPIGVPGEIF
IGGVGVARGYHGRPDLTAERFVPDPFGQTKGARLYRTGDRARWLPDGNLEFLGRNDEQVKVRG
VRIELEEIRAALLKHPAVAQAVAVVREDTPGDKRLVAYVVGRGGARVTAAELRQSVSERLPAT
MVPSSFVALDALPLTPNGKVDRRALPEPEQSAGGEDHVAPRNAVEEELARIWASVLRLERVGV
HDNFFEIGGDSILSIQIVVRAQQAGLRLTPRQMFQHQTIAELSTVARAVEAVHVEQDPVTGPA
PLTPVQRWWLEQEAAEPHHFNQSIFLEVRERLDESALEQAIAHLIDHHDALRLRLARDERGAH
QVFAAPGGSTPFQRVDLGALPSAEQISAMEKAASEAQASLDLAAGPVVRAVLFDLGEVAPQRL
LVIAHHIAVDSVSWRILLDDLFGAYEQARRGEAVRLPPKTTSVKRWAELLTEHAGSEAVKAEL
GYWLDSSRRTVAPLPVDRRAGEDVWGSARHIVVSLTPEQTEQLLREVPQAYRTRIDDALLTAF
AQAIARWTGSPAVLLDLEGHGREELAGVDLTRTVGWFTAMYPILLRVDAADPGEALKSIKEQL
RAVPGRGLGYGLLRYLRSDTIAEVRALPQAELCFNYLGQLDQAIPEAAPFRPAREYQGSERSP
GAHRAHLIEVNASIANGRLYATWTYSERRHEPETIERVAASFVTALRALIAHCTLPEVGGNTP
SDFDKVRLRQETIDALDAIDAGPGPSARGSRIEDVYPLSPLQEGILFHTLYATDYTAYVEQFH

WTLEGDFDAEAFTRALQDVVARHAALRTSFAWERLDAPLQIVRTGAVLPVEHQDLRGLAAEEQ
TAHISRYVEAERQRRFDLRKAPLMRAGLLRLRKDAWCLVETIHHLILDGWSTQILLKEVFTLY
EAHRGHRGHLALELEQPRPYGDYIGWLAKQDQVRTAAFWRRELEGFSAPTPLGVDRAVPHDDG
GPRFGWRRIALSGDDAARLAAFARQHQLTMSTLVQGAWALLLSRYSGDPDVLFGMTVSGRSAP
IPGIERMTGLFINTIPVRVREPADASVLAWLKALQEHEAELLEHEHSPLVEVQAHSDVPRGTP
LFESLVVFENYPVQVIFEAPPVEGPTRAEEGLRMIDAQYISDPPYPLTVVAAFHGTLYLNIGY
ERRRFDDQAVERMIGHVTTLLRGFVQRPETSVRDLPLLTAEEERTQLHAWNATAAPYPEGHCM
HELFEQQVERSPEATAVLLQQQTLTYRELNIRANQLAHHLRSLGVGPEVRVGLCLERSIETVV
AILGVLKAGGVYVPLDPTYPSERLGLMMEDAAPSVLLTQTSLLSKLPPHGDATLVQLDALHEA
LSRLPHHTPRSGVTAQNLAYVMYTSGSTGRPKGVLVEHRGLCNLPTVQAKLYAIAPSDRLLQF
APLCFDTSFCEIALALLSGATLVMGTADELLPGPPLVELLKKHAVTAMLLAPSVLAALPEQQS
AALPLRVLAMAGEACPAELVKRWKAPGRRLFNSYGPTETTIWASSAADLSDERIPPIGRPIAN
TQIYVLDEALEPVPIGVPGEIFIGGVGVARGYHGRPDLTAERFVPDPFGQTKGARLYRTGDRA
RWLPDGNLEFLGRNDEQVKVRGIRIELEEIRAALLKHPAVAQAVAVVREDAPGDKRLVAYVVG
RGGARLTAAELRQSVSERLPATMVPSSFVALDALPLTPNGKVDRRALPEPERSAGGEDHVAPR
NAIEEELTRIWADVLGAKRVGVHDNFFDLGGHSLLLVRVHDRLGQRFDRPPSMVDLFTYPTVA
SLARFLGERANGKQSPREAAADVTERGRRRLEARARRAKAIRGPT

SEQ ID No 28 (>ORF10)
MKHNIGWLLPAALATLAFVPACSPNHGEDAPSVTSAESGAAPSADCVALGAKLQAALDGAAAA
QKAPGAAAAVQSGDCVWRGATGVSDLVASTPTKPGDLFRIGSITKTFVSTLILMLRAEGRLSL
DDAVSKYVKGIPAGDQMTLRQILGHTSGLFDYTYSPALGQMIEVDPTRAFAPAELIALATAEA
PYFAPGAGFRYSNTNYIVAGLVAEAVSGGTLAGLLRTRILDPVGLAHTYLDGAEPPVQGLIRG
YGDYGAGLVDITDQLSPTEAWAAGALVSNVDDLNRFFALLISHELLSSDELQDMTTWTPTMWP
HEPGYGLGLIERDSALGSLNGHCGIIWGFQSASYGVPGRGDAITALINRSDGDAARLVDELAK
VVKER.

SEQ ID No 29 (>ORF11)
MSIDRAVLEQLDRVGGRLAEGKALKLLEDIAWPREVEERFFAAGEDRLPEVEYRVDRDGLARR
VAELRELLGAIDGDAPALGWLRDNVRAQIQAAELLEAAGTRAFSARSQELYGGARSRFFGGSL

RNIDLAEHLTERLRVHGWDEASDPEEEPLDAGALRDMLAARVAGRAPRLDLEITVDPRVTAKV
VAGMSRVRIRPEATFAAWEAEGLWHHEVETHALTAHNGAAQPRCAFLRSGGPRTTRTQEGLAI
FAELYSRSLSIGRLTRLAERVRLVDMAEQGASFLDLYRHLRERGAERRDAYFDAQRVCRGGLV
EGGAPFTKDACYLAGLLEVYAFLAAVLRGGLRDEVELLVCGRIALDDIAVLAELRAAGVLERP
RYLPGWLRAWQTLLPYFAFTSFMDGIDLGPVERHFQELLRVAADARPAGEGRRRRGRPREG

SEQ ID No 30 (>ORF12)
MSESVAQLEEHRAALTGHCYRMLGSVVDADDAVQETMVRAWRSLDKFDGRSSLRTWLYRIATN
VCIDLRADRARRARPIEEGPVGTVDDALETRPRTHWLEPVPDAHALPADIDAAERAMLRQSIR
LAFVAALQHLPPKQRAALLLTEVLGWSAAEVADSLNTSVAAINSALQRARATLASRDLGDARP
SLPEPQSALLDRYVNAFERYDVDALTALLHQDATLSMPPFTLWLRGHESIRAWLVGPGAGCRG
SRLIPTAASGSPAFAQYRPAPEGGHRAWALIVLDVAGDRIVSMTSFLDTETLFPRFGLPLDLP
A

SEQ ID No 31 (>ORF13)
VTIASIDHRDQDLMTGPQAKAPARAAAPDAAPSRRAVWAGRVLSGLATLFLTFDAAVKVLKLF
PAEASTAELGFPAHLVPTLGYLQIACLVAYLIPRTAVLGAILWTGYLGGAIAIHVRVENPLFS
HTLFPIYVAAFLWAGLWLRDRRVRALTASPSSQGR

SEQ ID No 32 (>ORF14)
MTTKNPRKLFVNLSVRDLKRSMEFFSKLGFEFNPQFTDEKAACMVVSEEAYVMLLVESFFKTF
MKKEICSTSTHTEGLFALSCSSRAEVDDMVKKAVAAGGSHAMDPQDHGFMYGWSFYDVDGHHW
EVMWMDPKAIQP

SEQ ID No 33 (>ORF15)
MTPSERLDATFAALADPTRRAILARLASGEASVTELAKPFAMSQPAISKHLKVLERAGLISRG
RDAQRRPCRIEAKPLEDASGWLDNYRRFWEGSYERLDDLLEELKERESKGERSKR

SEQ ID No 34 (>ORF16)
VAPASAPAAGGRDAAPFLDEAAQWLRGEQAPASRPAGEGPAGRLPGRVLVADDNADMREYALR
LLVAEGWTVEAVADGRAALERARAHPPDLVLTDVMMPRLDGFGLLRALRADDRTRGVAVVMLS
ARAGEEARVDSLEAGADDFLVKPFSAKELLARVRIHVELARRRREAEGQRQYLNDLFMQAPGP
IAILRGPEHVFEVVNPLYQRLVGGRSLVGEPIRAALPELEGQGIWELLDAVVRTGEPIVGKEL
PVRLDRRGDGTTEEVFFNFVYQPMRDRDGAVEGVFVFAFDVTDQVRARRRVEALVEALKLADQ
RKDEFLAMLAHELRNPMASISLSLTLLDDADGDGPASARYREIARRQMGHLVRLVDDLLDVSR
ITRGTVELRLEDVDLAAVVQSAAAAVRPAVEARRHDVSLSVGPGDFGMRADATRLEQVVTNLL
TNAAKYTPPGGSISVRLTREAAVGAPEAVLRVRDTGRGIPAAMLEKVFDLFTQVDQTIDRSTG
GLGLGLTLVRRLLELHGGSVAAASAGPGQGSEFTVRLPLGPGAAPQPAPSAGPPPPREGPPPA
QRDEPPPPPAQRAEAPEAAADRRRVLVVEDAEDVRRVMRAYIEALGHEVTVAVDGLEGVKKLL
ELRPEVAFVDIGLPGIDGYEVARRARAAPGGEALYLVALSGYGGPDDQARSRRAGFDLHLTKP
VVGATLQDVLTAPRT

9. DNA sequence according to claim 7 selected from the following

(a) open reading frames, and peptide sequences corresponding to said open reading frames:

pEPOcos6_ORF1 sequences:

(1) nucleotide sequence

Seq ID No 35 (>pEPOcos6_ORF1.seq)
GGATCACCTGCGGCGCGATCGCCGACCTCGTGCTGGTGTTCGGCTCGCTGGATGAGAAGCCGG
CGGCGCTACTGATAGAGACGGCGACGCCCGGGCTGCGGGTGGAGCGGTTGCGGGAGATGCTCG
GCTTTCGGGCGGCCCACCTGGCGAAGCTGTCCTTCGACGGTTGCGAGGTCCCCGAGGCTCAGC
TGATTGGCCGGCCCGGCTTTGCGCTGATGTATCTGGCCCCCTACGCCCTGGATTTCGGTCGGG
TCAGCGTCGCCTGGGCCTGCCTGGGCATGATCCGCGCTTGCCTGGAGACCTGCGCACAGCACA
TCCTCACCCGCCGCACCTTCGGCCACCTGCTAGCCGATCACGGCATGATCCAAACCCTGATCA

CCAACCTGGGGATTCACCACCAGGCGACGCTGCTCCACACGCTGCAGGCCTGCCGCGCCAGGG
ATCGCGGCGACGTGACCGCCTCCGAGGCCACCCTCGCCGCCAAATACCTCGCGTCGCGGACGG
CGGTCCAGGAGACGACCAACGCGGTCCAGATCATGGGCGCGCTGGGCTGCGACGAGGAGGGCG
CGATCGCCCGCCACTTCCGCGACGCCAAGACGACCGAAATCATCGAAGGCAGCAACCAGATCA
TCGAGGCGCTGCTGGCCAAGAACATCGCCCGCGCCGGTCGCGACAACTATCGCCGCTTCCTCG
ATGCGGAAGTCGAGCCCGGTCGGGCCGGAGGCGCACCA

(2) peptide sequence

Seq ID No 36 (>pEPOcos6_ORF1.pep)
ITCGAIADLVLVFGSLDEKPAALLIETATPGLRVERLREMLGFRAAHLAKLSFDGCEVPEAQL
IGRPGFALMYLAPYALDFGRVSVAWACLGMIRACLETCAQHILTRRTFGHLLADHGMIQTLIT
NLGIHHQATLLHTLQACRARDRGDVTASEATLAAKYLASRTAVQETTNAVQIMGALGCDEEGA
IARHFRDAKTTEIIEGSNQIIEALLAKNIARAGRDNYRRFLDAEVEPGRAGGAP*

pEPOcos6_ORF2 sequences:

(1) nucleotide sequence

Seq ID No 37 (>pEPOcos6_ORF2.seq)
ATGACGAGCGCGGTCCCGACGCGTCAAACCAGCCTGCTCGACGACTTCGAGCGCGTCGCCGAC
GTCGATCCAGAGCGGATCGCCGTCCACGCGAGCGAGACGAGCCTGCGCTATGGCGACATGAAT
GCGCGCGCCAACCGCATTGCCCACGGGCTACGGGCGCGCGGATCGGGCCCAATCAAATCGTG
GCGGTGGCGATGGCCCGCACGCCCGAGCTGATGATCGTGCTGTACGGCATCCTCAAGGCCGGC
GCGGCCTACATGCCCATCGCCCGCGACGCGCCGCCGCTGCGCCGCGATCATATGCTGCGCGAG
AGCCAGGCTGCTCTGATGATCGCCGACGAAGAGATCGCGGGACTCGCGGCCCGGGTGCTGACG
CCGGCCGACCCGTTCTTCGCGGCCATGCCGGACCACAACCCCGAGCCGCGTCACGACCCGACC
GACCTGATTTACGTCATCTACACCTCGGGCTCGACCGGCCAGCCCAAGGGCGTGGCCATGGAG
CACCGCGCCGTGTGGAATCGCCTGACTTGGATGCAGGCCCAGTATCCAATCGACACGCAGGAC
GTGATCCTCCAAAAGACGCCGATCGTCTTCGACGTGTCGGTCTGGGAGCTGTTCTGGTGGCCG
CTGGCCGGCGCCTCGGTGGCCCTGCTGCCGCAATCCATGGAGAAGTTCCCCTGGGCGATATCG
GCGACGGTGGCGCGGTGCGGGGTGACGGTGATGCATTTCGTACCATCGATGCTGATGGCCTTC

CTTCAGGTGGTGGCGGGCCGGCCCGAGATGGCGGACCAGATGAAGGGCCTGCGCTACGTCTTC
TGCAGCGGCGAGGCCCTGGCGCCGGCCCACGTGTCAGCCTTTCAGGAGCACATCAACCGAGCG
GGCAGCATCAGCTTGACCAACCTCTATGGACCCACCGAGGCGGCGGTCGACGTCAGCTACTTC
GACTGCCCGCCCGGCGCGTCACTCGCGCGGGTGCCGATCGGACGAGCGATCACCGGCATCCAG
CTGCTGGTCATGCGCGACGGCGTGCCTCAGCCGCCCGGCGTCGAGGGTGAGCTCGCCATCGGC
GGCGTTGGTTTGGCGCGCGGCTACATCTCACGGCCAGACCTGACCGCCGACCGGTTCGTGCCG
CATCCAGGCGGCGACGGCCAGCGGCTCTACCGCACCGGCGATCTGGTGCGCAGGGACGCGGAC
GGCGAGCTGGTCTTCCTGGGGCGCATCGACCATCAGGTGAAAATTCGCGGTCTGCGCATCGAG
CCCGGGGAAATCGAGGCCCAGATCAGCGCCCATCCCGATGTGGCCGACTGCGCGCTGATTATC
GAGCAGGACTCGGAAACCCTGCCCAAGCTGACCGCCTACATTGTCGTGGCGCGACCGGGCTTG
ACCCGGAAGGCGCTGCTACAGTTCCTGGGCGCGCGGCTGCCCGACTACATGCTCCCGAACCGC
TTCCTGACCCTCACGGAGCTGCCCGTGACCGCCAACGGTAAGCGCGACTGGCGCGCGCTGCTC
GGCCCGCTCGAGACCCTGCCTCTCCCTTTCTCC

(2) peptide sequence

Seq ID No 38 (>pEPOcos6_ORF2.pep)
MTSAVPTRQTSLLDDFERVADVDPERIAVHASETSLRYGDMNARANRIAHGLRARGIGPNQIV
AVAMARTPELMIVLYGILKAGAAYMPIARDAPPLRRDHMLRESQAALMIADEEIAGLAARVLT
PADPFFAAMPDHNPEPRHDPTDLIYVIYTSGSTGQPKGVAMEHRAVWNRLTWMQAQYPIDTQD
VILQKTPIVFDVSVWELFWWPLAGASVALLPQSMEKFPWAISATVARCGVTVMHFVPSMLMAF
LQVVAGRPEMADQMKGLRYVFCSGEALAPAHVSAFQEHINRAGSISLTNLYGPTEAAVDVSYF
DCPPGASLARVPIGRAITGIQLLVMRDGVPQPPGVEGELAIGGVGLARGYISRPDLTADRFVP
HPGGDGQRLYRTGDLVRRDADGELVFLGRIDHQVKIRGLRIEPGEIEAQISAHPDVADCALII
EQDSETLPKLTAYIVVARPGLTRKALLQFLGARLPDYMLPNRFLTLTELPVTANGKRDWRALL
GPLETLPLPFS

pEPOcos6_ORF3 sequences:

(1) nucleotide sequence

Seq ID No 39 (>pEPOcos6_ORF3.seq)

ATGTTACACCCGATTCCCACCGACCGTTTCGCCCTGAGCCGACCGCTCTTTCGCGGGTACCTC
GCGCACGATCCGATCGTGCAGGGCGTGCTGGCGGGCGACCATCCAGGCTGGGTCCTGGTGGAC
CGCGAGCCCGAGCCGCGCACGGCGCTGCTGTGGGCCTTTTCCGATCGGCTCTTCTGCGTGGGC
GCAGCTGACACGCTGACCCCGCACGCGCTGGCCGAGCTGTTCCACGACCGACTGATCCCCCAG
GCCCGTAAGATCGGGCAGCCGTTTTTCCAGGTTCAGGGCGAGACGGTCGACACCTGGTCGGAC
CACCTGCATCAGGTGTCGCCGCACGCGACAGTCTCCTTCCGCCAGGCATTCCGCTTCGACCGC
GACCTCTTCGAGCGGCTGCCAACCAAGCCGGAGCTGGCAGAGGCGCGGCTCGTGCCAATCGAC
GCGCGGCTGCTGGCCGAACAGGCTGATCTGCGCGAGCGGATACTGGCCTCCTGGTCCAGCGAA
GCTGCCTTCCATGCGCGCGGTTTCGGCTTCTGCTACCGCGTAGGTGACCAGCTGCCGAGCGTG
TGCCTGGCATCGCACGTAGGCGGCGGCGCGGCCGAGCTGAGCATCAACACCGAGCTCGAAGCG
CGCAATCGAGGTATGGCAACGCGGCTGTGCCGGCGTTTCATCGCCGAATCGCTGCAGCGCGGC
CTGACGCCTTGCTGGGGCACCGAGACCTTTCGCCTGCCGTCAATCGCGCTGGCCCAGAAGCTC
GGTTTCATCCCGACCTTCACCTTCCCCACCTACTGCTTCGCGACCGGCACCGAACAGCCGGAC
GACAACTTCCTAGGCGAGCTGTACTACAGGGAATCGCGCATCGCCGGAAGTGGGACCGATGAG
CCGCAAGCGGTTCGGCTGGCGCGGGGTTGGAGCCTGGCCGGCGACACCGAGCGTGCCGCGAGC
TTCGCCGCACGCGCCCTGGCCGAAGGGTGGGCCGGCCACTCGACTCTGGCCACCGATCCGGAT
TTCGCCCGATTGCGCGCCAGCGCCGCCTGGCCCCGCCTCAATGTCCCT

(2) peptide sequence

Seq ID No 40 (>pEPOcos6_ORF3.pep)

MLHPIPTDRFALSRPLFRGYLAHDPIVQGVLAGDHPGWVLVDREPEPRTALLWAFSDRLFCVG
AADTLTPHALAELFHDRLIPQARKIGQPFFQVQGETVDTWSDHLHQVSPHATVSFRQAFRFDR
DLFERLPTKPELAEARLVPIDARLLAEQADLRERILASWSSEAAFHARGFGFCYRVGDQLPSV
CLASHVGGGAAELSINTELEARNRGMATRLCRRFIAESLQRGLTPCWGTETFRLPSIALAQKL
GFIPTFTFPTYCFATGTEQPDDNFLGELYYRESRIAGSGTDEPQAVRLARGWSLAGDTERAAS
FAARALAEGWAGHSTLATDPDFARLRASAAWPRLNVP

pEPOcos6_ORF4 sequences:

(1) nucleotide sequence

Seq ID No 41 (>pEPOcos6_ORF4.seq)

ATGATTTGTCACTCCCACCGCTTCATTTTCCTCCACGTTCCCAAGGTCGCCGGCACAAGCGTC
AAGGACGTCCTCGGCCAAGAGCTATTCCAGGAGGACCAGGTCACGTTCCAGATCGCTCCCAAT
CCCCACTACCCACCTGAATGGACTGCGCCTTACGAGGAGCACATTATTGCCGCTGAATTGAAG
AGCCAGTTGGCGCCGGAAATTTGGGACGATTACTTCAAGTTCGCCTTCGTGCGCCATCCGCTC
GACTGGGCGGTCTCCAATTACTTCTTCTTCCTGCGCGACCGCAAAGGCCATCCGGCCCACGAA
TTCCTGGAGCGGAAGGGCTTCGCCGGTACCATGGACATGTTTTTCGGAGCGGCCGGGCGCCAT
CCGCTGGTCGCCGGCATGCGCTTCAGCCAATGGGAGTTCTTGTGCGACAGCGAGGGCCGGACG
CTGGTGGACTTCGTTGGCAAGTACGAGCGGCTCGAGCAGGACTTCGCCGCCGTGTGTATCCGC
ATCGGGCTGACCCCGCCCGACTTGCCGTGCCTCAACCAGACTCGCCACCAATCCTTTACCAGT
TACTACGACGAGGCTTTGATGCGCCAAGTCAGCCGCGCGTTAGCTCGCGATTTCGAAATTTTT
GATTATGCC

(2) peptide sequence

Seq ID No 42 (>pEPOcos6_ORF4.pep)

MICHSHRFIFLHVPKVAGTSVKDVLGQELFQEDQVTFQIAPNPHYPPEWTAPYEEHIIAAELK
SQLAPEIWDDYFKFAFVRHPLDWAVSNYFFFLRDRKGHPAHEFLERKGFAGTMDMFFGAAGRH
PLVAGMRFSQWEFLCDSEGRTLVDFVGKYERLEQDFAAVCIRIGLTPPDLPCLNQTRHQSFTS
YYDEALMRQVSRALARDFEIFDYA

pEPOcos6_ORF5 sequences:

(1) nucleotide sequence

Seq ID No 43 (>pEPOcos6_ORF5.seq)

ATGAAAGTGGACAAGCGGAATGTCGACGACATTCTCGGACTCACTCCGACACAGACAGGCATC
TTGTACCACTACCTGCTGGACCCGCAGGCCGACGCCTATTTCGAACAATTGACGCTGCACCTG

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GAGGGGCCGCTCGACGTAGCGCGCTTCCGCCGCGCCTGGGAGCGCGTGGTGGCGGCTCACGAC
CAGCTGCGCGCCGTGTTTCGCTGGCAAGGGATCGAACACCCGGTGCAGATCATCCTCAAGCAG
CACGTGCCGGACCTGGAGTTGGCGGAGGTCCCGCGCGACGCCGATCCGGCAGCCTTCCTGGCG
CAATGGGTCGCGGCCGACCGGGCGCGCAAGTTCGACTTCGAGACGGTGCCCTTTCGCATCGGC
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GGTTGGAGTACGGGCCTGATTCTGCGGGACTTCCTCGCCTGCTACGGCGACTCCGAAAACTGG
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GGCGAGGAGCGATTTTGGCGCGACCTGTTGCGCGATGCGCCCGACGGCGGCTTTCCCCGCCTG
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CGCTTGACCCAAGGCTTGCGCGACATGGCTCGCGACCTCGACGTCACCCTCGCCGCGATGCTC
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CGCCGTGACCTGCTGGGCGACGCGGCCGCTGAGCGAATGCTAGATCATTTCACCGGCCTGCTC
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GCCCACCGCGTCCTGCACCAACTCAACCAAACGCGTCAGCCGCTGCCGTCCCAATCGGCTTTC
CACCAGTTGTTCTTCGAGCAGGCCCAGGCCGATGGGGCACGACCGGCGCTGTGGTGCGGCGCC
ACGCGCTGGACCTACGGCCAGCTGCTGGAACGTGCCCTGCGTCTGGCGGGACGGCTGCAGGAA
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CAGCGCTCGCGGTTCATCCTCGACGATGCCGGTTGCCGCTTCCTGATCAGCGACGCGCCACTC
GCGGGGCCCACGCCGATCCATCCGGACCCTGCCGGCGCCAGCCCCGTTGACGTCATTTTTGCC
TGTCAGGACGGCGCCGCGCAGCCCGCCTACCTGATCTACACCTCGGGCTCCACCGGCCAGCCC
AAAGGCGTCTGGGTTAGCCACCGCAACCTGATCAACTTCCTGACGGGCATGAGCGCAATCCTG
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GACCCGGCCGCGGCTGCCAAGGCCATCTCCTGCCATGGCGTCACGGTTTACCAGGCGACGCCA
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CGGGCCTTCGACGCCCAGGCGGCCGGCACGGTCTGCGGCAACGGTCTGGGCATGGTGGTGCTG
AAACAGCTCGACGCGGCGCTGGCCGACGGCGATGCCATCCACGCTGTGATTAAGGGCATCGCG
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CAGCTGTTCGCGACCCTGTCGGCCGAAGCGATGCTGCCCACCCACATCCTGCACCTGCTCAGC
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CACCATCTGCTGGCCCTGGCCCGCCAACTGGAGGCGGTCGGCGCCCCCGAGGTCCGCCTCGCC
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CGCACGCGCGCTGCCAGCGACGCCGTGCTGGCGCCCAAAACGGTCGGAACCTGGATTCTCGAT
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GCGCCCTTCGGCCAGGTTGCCTACGCCGCCGCCAACGCCTTCCTCGACGCCTTCGCCAGCGCC
CACGAACACGACGAGCGTCTTTTCCGCGTCAGCATCGGTTGGGACACCTGGCGCGAGGCCGGC
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TTGGGCCGCGATGTCCCTGTCGTCTCGCTCTACCAACACCGCACCGTACGCGGGCTGAGCCGC
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TTCCTCGGCGGCGCGCTCCAATCCGCGCGGTCCGGCGTCCCGACGGGCGCTGCCGCACCGGGC
GCCGCCACGCCGGGGGTTGCCACCCCGCCGCGGCCACAACCGTCGCGCCAGCACCTGGAAAAA
CGCCGTCAATTGAGGAAAAAAGGGGGGCCTTCCCATCATGAG

(2) peptide sequence

Seq ID No 44 (>pEPOcos6_ORF5.pep)

MKVDKRNVDDILGLTPTQTGILYHYLLDPQADAYFEQLTLHLEGPLDVARFRRAWERVVAAHD
QLRAVFRWQGIEHPVQIILKQHVPDLELAEVPRDADPAAFLAQWVAADRARKFDFETVPFRIG
LCRTDTQHHVMLLSNHHILMDGWSTGLILRDFLACYGDSENWRPRTRTHFKAFIKWHQNRPRR
GEERFWRDLLRDAPDGGFPRLGVEEGTRHSLDFGARSRALDDRLTQGLRDMARDLDVTLAAML
HTAWGLLLQRYQNSCEVIFGTTVSGRNVELAGLDEVVGLFINTIPFRFSAAAATTPVEAFRAV
QRNLLARSEFEATPLVDIKGWSGLGPGAELFDTILVIENYPLDRAIFESDSSLRLTDHQIFER
TNYGLTLTIETFSRLHVTLAHRRDLLGDAAAERMLDHFTGLLQAMLRFPHQPFARLEMKSEHE
AHRVLHQLNQTRQPLPSQSAFHQLFFEQAQADGARPALWCGATRWTYGQLLERALRLAGRLQE
AGFARGDVAAVSLGPVPDLIPGLLGPLFAGGAYLPLDPTLPAQRSRFILDDAGCRFLISDAPL
AGPTPIHPDPAGASPVDVIFACQDGAAQPAYLIYTSGSTGQPKGVWVSHRNLINFLTGMSAIL
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SRLQLQLEHPTFVRAIGSLTTLLVGGEPLPAELLRRVREVTDARIFNLYGPTETTIWSTAGEV
TAADVPDIGRPIANTGVFLLARDGSIQPPGLVGELCIAGEGVALGYHRRPDLNRERFREIPPG
RLPFAGKLYHTGDLARWTEDGRLLCLGRLDDQLKVRGHRVEPGEIEAVMARHPAVTQAVVVTR
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FALTESTRQAAPRTLARTAGEHRVAELWQALLRREAIGLDEPFFQAGGNSFGLIRLHAKLESA
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SGLTAQPPQPHFRPIAVIGLAGRFPAAPDLDAFLELLTEGRCGIRFFSQAELRDEGLDANRIA
CHNYVPAKGFLDRADHFDADFFGIPPRDAEITDPQIRLLLECCWNALEHAGYPPGGGEIGLFA
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ACDALHAGRVTMALAGGVGLTYPLRAGYLHEDGMIFSPDGRCRAFDAQAAGTVCGNGLGMVVL
KQLDAALADGDAIHAVIKGIAANNDGAAKIGYTAPSQNGQARVIRAAHRLAQVAPETIGYVEA
HGSGTPLGDPIEVAGLTEAFDSPRRGFCALGSVKSNVGHLDAAAGIAGFIKAVLSLSHRTLFA
SLHVDTPNPQIPFADGPFQVNTETRPWPAADHPRRAGVSSFGIGGTNVHAVLEEAPQLAEHAG

RRRERQLFLVSARTAADLERRTAALVRHLAAHPDLAPDDVAFTLHAGRKPMTHRRFLVAADLA
EAAARLAEPDPVKSAAARADRCQVWMFAGLGSQYPGMCGGLYRTEPAFREQVDRCFDLLAPRC
DLKPSLFPEPDQAIDASALAAIDTAQIAVFVCEYALARMLEGWGLRPDRLIGYSFGEYVAACL
AGVFSLPDALAIVRERGRILAAAEPGAMVSVPLPAERVASLLEPPLALAIDNGPSCVVSGPVE
PVRTFTARMKRDRVWVTPLQAERPMHSPLMAEAGGSLRAMLAGFRLNAPRIPILSNVTGTYLT
DEQARDPDYWARHLCGNVRFADGVRTLLAERDPVFLEFGPGRDLSSLVRHQMPEGADEPIALI
RHREDPVRDEDLLLDGLGRCFLRGATLHGQALYAGRGCRRVPLPGYPFQGPRCMPARAGLPGL
ARPTVGATTISYRPAWKRAPRLAAVESLAPQSWLVFSDGSELAGELVAGLRASGCATTLVEGG
LAFARFAGGFRANPREEQDLAQLFATLSAEAMLPTHILHLLSLPSPERDSPLARLEHLTELGF
HHLLALARQLEAVGAPEVRLAVVTTGLAAIGGESELRPEVGLLRGPVRVIPFEFPNLRLRLID
LDSADPIWRSGCEPLLREMGAAPGPEEIALRGTSRWELGYEPVEGGTVSTISSRLREGGVYLI
TGGLGGLGLALARHLARKYRATLILAGRRGAPARELWHQAPAEFVPVAAAIAQMEECGARVIP
VALDVTDADQVNALFATIEATVGKIEGVFHMAGIVDGGIIRTRTRAASDAVLAPKTVGTWILD
RALRGAGGRFLVLYSSINAVVAPFGQVAYAAANAFLDAFASAHEHDERLFRVSIGWDTWREAG
MAVDAARARGDQAPLEGLSDEQGLRLLESALVGCEPRLLVSISELRARLAEHHRNGGIPRLLG
PRANEAGAADSGEEGATQDASPARRARPDLVVAFAPAGNELERRIVAIIGAYLRLGQVGVDDN
FNDLGATSLDLIQIAQRLGRELGRDVPVVSLYQHRTVRGLSRFLGGALQSARSGVPTGAAAPG
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pEPOcos6_ORF6 sequences:

(1) nucleotide sequence

Seq ID No 45 (>pEPOcos6_ORF6.seq)

ATGAGTGAAGTATCCATTCGCCCCGGCTTGGACATCGCGGTCATCGGCATGGCCTGCCGCTTT
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GCGCTGGAGCACGCGGGCTACAACCCGCATCGCCACACCGGCACGATCGGCCTGTTCGCCGGC
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TGGGATCACGAGCCGCTTTATCGCGCGGCGGCGACGTCGTGCTTGGCTGGTGAGGTCGCCGAC
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CACCAATACGCGCTGGCCGGATGGCTGCTGGCCATGGGGTTGACCCCGTCGGCGTTGATCGGC
GTGGGCCAGGGCGAGTGGGTAGCAGCGGCGCTCGCGGAGGTGTTCCCGCCATCGGCCTGCTTG
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(2) peptide sequence

Seq ID No 46 (>pEPOcos6_ORF6.pep)

MACRFPGARNLAEYWANLIEGLETLSFFSEEELREAGCDPVQLAQHNYVRTKGLLPDADRFDA
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SVSITLPLVAGYTYTPGMIVSPDGHCRTFDAGANGTVYGDGAGVVVLKRAEDALADGDHIFAL
IKGSALNNDGSRKTGYTAPSVQGQVEVIRAAMNLAEVEPEAISYVETHGTGTTVGDPLEFEAL
KEAFGGGCKAFCGLGSVKPNIGHLDVTSGIASFIKLVLALEHRILPPTLHFQLPNPKMDVVDS
PFYIVAEREPWREDLLPRRAGVSAFGLGGTNVHMILEEFQREPAANSARTRHLTVLTARSPQA
LAQLAANLAEHLREHPELALADVAHTLLHGRKPHPFARILVATDTTAAIDALMNDRDPRTRFF
EATGRGESVILCFDETPPEPRSARYLWDHEPLYRAAATSCLAGEVADPDLEGCFTALIAEQGA
AAAFCHQYALAGWLLAMGLTPSALIGVGQGEWVAAALAEVFPPSACLRWIRFGERLPQPRDQR
IPFLSNFSGNWIVGRELADPDYPRKQKGKRCMKRRRSQPRSAGAGWGRWNRLGQLVARCSSAG
SGGGTVIGPRARFISSSTSRARVRAQYLGASSR

pEPOcos6_ORF7 sequences:

(1) nucleotide sequence

Seq ID No 47 (>pEPOcos6_ORF7.seq)

ATGGAACCGGCTCGGTCAGCTCGTCGCGCTGCTCTTCCGCGGGAAGCGGAGGCGGGACGGT
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CAGGTAGGCCTCCGGGTCGAGCCCGTGCAGCTTGCAGCTCGCCACGAGCGAGAAGAGGTTGGC
CGCGGCGGAGGCGTGGTCGTCGCTGCCGAAGAAGAGCCAGGACTTTCTCGCAACCGCAATGGA
TCGCAGCGCTCGCTCGCTGGCGTTGTTCTCCAGGCGCAGCCGACCGTCGTCGAGGAAGCGCCG
CAACGGCTGCTCTTGGTTGAGGGCGTAGCCGAGCGCGGTGGAGACCAGGCCGCGCTCGCGGGG
ACGAGCGTGCTCGGCCCTGGCCCAGGCAAAGAACGCGTCGACCAGAGGGCGGACGACGACATC
GCGACGCACCTTGCGCTGCGCGGCGGCAGGTCCGCCAGCGCGCGATCGGCGGCAAAGAGGGC
GTTGATGCGCCGCAGCCCCTCGACACCGAGCTCGTGCTTGCAGACCGCCGCCTCCCAGAAGTT
GGTACGGCAATGCGACCAGCATCCGACTTCGGTCGGGGGCGGACCGCGCTTCTCGTCGGCAGC

AGCGCCTCTTGGTGGTGTGCCGCGGAAGAGGGCGTCATAGATGGCGTGAGCGTCAGCTTGAAT
ATACCGAGAGAAGCCGCGGAACATCTCGCAGACCGCGGCGCTGGTATGCTTGGGCTGGTACTC
GAAGAAGACGTGATCCTTGTCCGCGAGGACGACGAAGAAGTGTCCCTTGCGGCACGGCCCGGG
CTTCTTGTCCTTGCGCTCCTGGATGGGCCCAGGCTGGACGGAGACCCCGGTGGCGTCCGTGGA
CAGGCAGAAGGCGGTCTCGAAGGCCTCTTTGCGCGCGGCCTCGACGATGGCGCCCAGGGTCGC
ACCGACGTCTTCGGCGTAGCGGCACATCGTGCCGCGATCGAGCGACGCGCCCTGAAGCTCCAG
CTGCTGCTCCAGTCGATAGAACGGGACGCCGAGCAGGTACTTGCTGGTGAGGATGTGCGCAAT
CATCGACGGCGCGAGGAACGACCGCCGGAACAACTCCTTCGGAAGCGGCGTCGTGATGAAGAC
CGTGCAGGTCTCGCCCTTCGGCGCCGGCGGCGCGTCGAGCGAGGGCGCGTCGAGCGCTGT
GGAGGAAGCGCTCGGCTCGCCGGCCGCTGCCGTGTCCTCCGGGCTGACGCTCGCAGCGGGCGT
CGGCGTCGGGGCTTCTCTCGCGACGACCTGGAGCGGGGCCGCTTCCTCCTCGCCCGAACTGCT
CGCATCCGTGACGGACCGCTCGGCCTTGTACACGACGCGTGCGAGCACGATGCGGCGCATTCC
GCCGCGCTCGTAGCCGAGTCGCGAGGTCTCCTCGACCCCGATGCGCGTCGCCGTCGCATCGAG
CTCGGGGCAGGAGAGCTCGATGCGGACGACGGGCAGGTCGGACTCGGACAGGTCGCGACGGCC
CTTGCCGCCGGACCTTCGTTTCGGCCCCTTGGGGTCGTCGTGCTGCCGCTCGTCGCCTGTATT
GCGCTCGGCGGCGTCGAGTGCCTTCGCGAGGCGCTGGACCTCGAGGAACATCGAGTCGAACGC
CAGCTGCTCCGCGCTCACCTCGGCGCGCTCCGCCTTGGCCACGAACAGTCGACGTCGCAGAAG
CTGCAGCTGCTCGAGCGCACGGGTGTAGGCGCGCCGAAGCTGCGCGAGCGCATCGCGCGCTCC
CACGAGCTCGCTCTTTGCCGCGGCGAGCTCCGCTTCGAGCTGCGCGATGCGCTGCTGCTCGGC
CGAGAGCGTCGGCTTGGCGGCGGCGTCGTGCACGACGCCGCTCTACGTAAGCCGCGCGTACTT
GTCGAGCGAATTCGTGCGGCTCAGTGGACGCGGCGCGGTGCGCGCCTTCGCGGTTTGGACGTG
GGCGCGATCTCGATGCCGTCGAGCAGCGTCTCGAGCGTGGCGTCGTCCACCTCGACGTGCGTG
GCGCCCTCGGTCGGGGGGTCGGGAAGTGCGAACGCTCCGCGATCAAGGCGTTTTGAAAACAGG
CAGATTCCACTGCCATCGAAGAAGAGAATCTTGATCGTGGTCCGCCGCTTGCCGACGAACGCG
AACAGCGCTCCGCAGCGAGCCTCGTACCCCACACGCTCACGGATGAGACCCGAAAGCCGCTCG
AAGCCG

(2) peptide sequence

Seq ID No 48 (>pEPOcos6_ORF7.pep)

MEPARSARRALLFRGKRRRDGDRPEGEVHLVVDEPGAGARPVPGGELEVAVPRPVGHRANDVG
QVGLRVEPVQLAARHEREEVGRGGGVVVAAEEEPGLSRNRNGSQRSLAGVVLQAQPTVVEEAP
QRLLLVEGVAERGGDQAALAGTSVLGPGPGKERVDQRADDDIATHLALRGRQVRQRAIGGKEG
VDAPQPLDTELVLADRRLPEVGTAMRPASDFGRGRTALLVGSSASWWCAAEEGVIDGVSVSLN
IPREAAEHLADRGAGMLGLVLEEDVILVREDDEEVSLAARPGLLVLALLDGPRLDGDPGGVRG
QAEGGLEGLFARGLDDGAQGRTDVFGVAAHRAAIERRALKLQLLLQSIERDAEQVLAGEDVRN
HRRREERPPEQLLRKRRRDEDRAGLALRRRRRRVERGRVERCGGSARLAGRCRVLRADARSGR
RRRGFSRDDLERGRFLLARTARIRDGPLGLVHDACEHDAAHSAALVAESRGLLDPDARRRRIE
LGAGELDADDGQVGLGQVATALAAGPSFRPLGVVVLPLVACIALGGVECLREALDLEEHRVER
QLLRAHLGALRLGHEQSTSQKLQLLERTGVGAPKLRERIARSHELALCRGELRFELRDALLLG
RERRLGGGVVHDAALRKPRVLVERIRAAQWTRRGARLRGLDVGAISMPSSSVSSVASSTSTCV
APSVGGSGSANAPRSRRFENRQIPLPSKKRILIVVRRLPTNANSAPQRASYPTRSRMRPESRS
KP

pEPOcos6_ORF7.1 sequences:

(1) nucleotide sequence

Seq ID No 49 (>pEPOcos6_ORF7.1.seq)

ATGTTCCTCGAGGTCCAGCGCCTCGCGAAGGCACTCGACGCCGCCGAGCGCAATACAGGCGAC
GAGCGGCAGCACGACGACCCCAAGGGGCCGAAACGAAGGTCCGGCGGCAAGGGCCGTCGCGAC
CTGTCCGAGTCCGACCTGCCCGTCGTCCGCATCGAGCTCTCCTGCCCCGAGCTCGATGCGACG
GCGACGCGCATCGGGGTCGAGGAGACCTCGCGACTCGGCTACGAGCGCGGCGGAATGCGCCGC
ATCGTGCTCGCACGCGTCGTGTACAAGGCCGAGCGGTCCGTCACGGATGCGAGCAGTTCGGGC
GAGGAGGAAGCGGCCCCGCTCCAGGTCGTCGCGAGAGAAGCCCCGACGCCGACGCCCGCTGCG
AGCGTCAGCCCGGAGGACACGGCAGCGGCCGGCGAGCCGAGCGCTTCCTCCACAGCGCTCGAC
GCGCCCTCGCTCGACGCGCCGCCGCCGGCGCCGAAGGGCGAGACCTGCACGGTCTTCATCACG
ACGCCGCTTCCGAAGGAGTTGTTCCGGCGGTCGTTCCTCGCGCCGTCGATGATTGCGCACATC
CTCACCAGCAAGTACCTGCTCGGCGTCCCGTTCTATCGACTGGAGCAGCAGCTGGAGCTTCAG

GGCGCGTCGCTCGATCGCGGCACGATGTGCCGCTACGCCGAAGACGTCGGTGCGACCCTGGGC
GCCATCGTCGAGGCCGCGCGCAAAGAGGCCTTCGAGACCGCCTTCTGCCTGTCCACGGACGCC
ACCGGGGTCTCCGTCCAGCCTGGGCCCATCCAGGAGCGCAAGGACAAGAAGCCCGGGCCGTGC
CGCAAGGGACACTTCTTCGTCGTCCTCGCGGACAAGGATCACGTCTTCTTCGAGTACCAGCCC
AAGCATACCAGCGCCGCGGTCTGCGAGATGTTCCGCGGCTTCTCTCGGTATATTCAAGCTGAC
GCTCACGCCATCTATGACGCCCTCTTCCGCGGCACACCACCAAGAGGCGCTGCTGCCGACGAG
AAGCGCGGTCCGCCCCCGACCGAAGTCGGATGCTGGTCGCATTGCCGTACCAACTTCTGGGAG
GCGGCGGTCTGCAAGCACGAGCTCGGTGTCGAGGGGCTGCGGCGCATCAACGCCCTCTTTGCC
GCCGATCGCGCGCTGGCGGACCTGCCGCCCGCGCAGCGCAAGGTGCGTCGCGATGTCGTCGTC
CGCCCTCTGGTCGACGCGTTCTTTGCCTGGGCCAGGGCCGAGCACGCTCGTCCCCGCGAGCGC
GGCCTGGTCTCCACCGCGCTCGGCTACGCCCTCAACCAAGAGCAGCCGTTGCGGCGCTTCCTC
GACGACGGTCGGCTGCGCCTGGAGAACAACGCCAGCGAGCGAGCGCTGCGATCCATTGCGGTT
GCGAGAAAGTCCTGGCTCTTCTTCGGCAGCGACGACCACGCCTCCGCCGCGGCCAACCTCTTC
TCGCTCGTGGCGAGCTGCAAGCTGCACGGGCTCGACCCGGAGGCCTACCTGGCCGACGTCATT
CGCGCGATGCCCTACTGGCCGCGGGACCGCTACCTCGAGCTCGCCCCCAGGTACTGGGCGCGC
ACCCGCGCCCGGCTCGTCGACGACGAGATGAACCTCGCCCTCGGGCCGATCACCGTCCCGCCT
CCGCTTCCCGCGGAAGAGCAGCGCGCGACGAGC

(2) peptide sequence

Seq ID No 50 (>pEPOcos6_ORF7.1.pep)
MFLEVQRLAKALDAAERNTGDERQHDDPKGPKRRSGGKGRRDLSESDLPVVRIELSCPELDAT
ATRIGVEETSRLGYERGGMRRIVLARVVYKAERSVTDASSSGEEEAAPLQVVAREAPTPTPAA
SVSPEDTAAAGEPSASSTALDAPSLDAPPPAPKGETCTVFITTPLPKELFRRSFLAPSMIAHI
LTSKYLLGVPFYRLEQQLELQGASLDRGTMCRYAEDVGATLGAIVEAARKEAFETAFCLSTDA
TGVSVQPGPIQERKDKKPGPCRKGHFFVVLADKDHVFFEYQPKHTSAAVCEMFRGFSRYIQAD
AHAIYDALFRGTPPRGAAADEKRGPPPTEVGCWSHCRTNFWEAAVCKHELGVEGLRRINALFA
ADRALADLPPAQRKVRRDVVVRPLVDAFFAWARAEHARPRERGLVSTALGYALNQEQPLRRFL
DDGRLRLENNASERALRSIAVARKSWLFFGSDDHASAAANLFSLVASCKLHGLDPEAYLADVI
RAMPYWPRDRYLELAPRYWARTRARLVDDEMNLALGPITVPPPLPAEEQRATS

pEPOcos6_ORF7.2 sequences:

(1) nucleotide sequence

Seq ID No 51 (>pEPOcos6_ORF7.2.seq)

ATGATTCCGGCGGGCGTGCAGGTGTTCGTCGCGCTGGAGCCGGTGGACATGCGCTACGGCTTC
GAGCGGCTTTCGGGTCTCATCCGTGAGCGTGTGGGGTACGAGGCTCGCTGCGGAGCGCTGTTC
GCGTTCGTCGGCAAGCGGCGGACCACGATCAAGATTCTCTTCTTCGATGGCAGTGGAATCTGC
CTGTTTTCAAAACGCCTTGATCGCGGAGCGTTCGCACTTCCCGACCCCCCGACCGAGGGCGCC
ACGCACGTCGAGGTGGACGACGCCACGCTCGAGACGCTGCTCGACGGCATCGAGATCGCGCCC
ACGTCCAAACCGCGAAGGCGCGCACCGCGCCGCGTCCAC

(2) peptide sequence

Seq ID No 52 (>pEPOcos6_ORF7.2.pep)

MIPAGVQVFVALEPVDMRYGFERLSGLIRERVGYEARCGALFAFVGKRRTTIKILFFDGSGIC
LFSKRLDRGAFALPDPPTEGATHVEVDDATLETLLDGIEIAPTSKPRRRAPRRVH

pEPOcos6_ORF7.3 sequences:

(1) nucleotide sequence

Seq ID No 53 (>pEPOcos6_ORF7.3.seq)

ATGACAAGGACGAAGGCGACCGAAGTGATGTGGTCCGAGCGCGTTCGGGCGTGGCGCGAGAGT
GGTGAAACGGCGGAGGAGTTCGCTCGGAGCCGCGGATTTGCGGCCTCGACGCTGCACGGCTGG
TCGAGCCGGCTGTCGCGGGCCGAGCCACCGCGCTTTCTGCGCCTGGTGCCGAAGGCGCCCGCC
GTGACGAGCAGCGCTGCGGAGCTCGTCGTCGAGGTCGGCGGCGCGCGGGTGCGCGTCGCCGCG
GGGTTCGACCCCGCGCTGCTGGCGGAGGTGGTCCGTGCCCTCGGCGGAGCGGGGCGA

(2) peptide sequence

Seq ID No 54 (>pEPOcos6_ORF7.3.pep)

MTRTKATEVMWSERVRAWRESGETAEEFARSRGFAASTLHGWSSRLSRAEPPRFLRLVPKAPA
VTSSAAELVVEVGGARVRVAAGFDPALLAEVVRALGGAGR

pEPOcos6_ORF8 sequences:

(1) nucleotide sequence

Seq ID No 55 (>pEPOcos6_ORF8.seq)

ACTGGACAGCGCAGCCGGGGTGAGACGGCGCTTCGCGCAGCGCTTACGCAGAAGGCGCGCCGC
GCGCCATTGTCGGATGCGGTGCGCGACTTCGCCGCCGATCGGCTGTTGCTGGAACTGGGACAA
CCACTGGACGTAACGGCTGAAGCGAGCCAACGGCTCCAGCTCGCGCGGGGCGACCTGTTCGGC
GCCTACCAAGCGTTGGCCCAGCTCTGGATCTGCGGCGCCCTGGCCGAACCGCCGCGACTGTAT
CCCGACGAACACCGCCGGCGCGTGCCGCTGCCGAGCTACCCCTTCGAGGGAAAGCGGTTCTGG
ATCGAGGGCTCGCCGTTCGAAACCGCGCCCGCCGCCGGCGCCTCACCCCAACCCGCCGATTCG
GGGGACATTCTCAAGGGCGACCCGGCGGACTGGTACTATCGGCCGCGTTTCGAAGCGGCGCCG
CTCTTGCCCAGCCCGTTCGAGAGCGAACCCGGCGATTGGCTGGTGTTCGAAGATGAGCTGGGG
CTCGGCGCCTGGCTGAGCGAGACCTTGCGCGACAAGGGCGCGCGGGTCGCGACAGTCGTTCGA
GGCACCGAGTTCCGACGCCTGGCGTCACAGCGCTTCCAGCTTCGTCCCGATCGACGGGACGAT
TACCGGACCCTGCTGCACGAGTTGAAGGCGCAGGGCATCGCGCCGGTCCACCTGTGCCACCTA
TGGAGCGTGACCGCCGCACCGGATGCCGAGCAGTTGCTCGACGTCAGCTTTCACAGCCTGGTC
CATTTGGCGGCCGCTTTGGGTTCGGTTGGCTACTTCCACGCCATG

(2) peptide sequence

Seq ID No 56 (>pEPOcos6_ORF8.pep)

TGQRSRGETALRAALTQKARRAPLSDAVRDFAADRLLLELGQPLDVTAEASQRLQLARGDLFG
AYQALAQLWICGALAEPPRLYPDEHRRRVPLPSYPFEGKRFWIEGSPFETAPAAGASPQPADS
GDILKGDPADWYYRPRFEAAPLLPSPFESEPGDWLVFEDELGLGAWLSETLRDKGARVATVVR
GTEFRRLASQRFQLRPDRRDDYRTLLHELKAQGIAPVHLCHLWSVTAAPDAEQLLDVSFHSLV
HLAAALGSVGYFHAM

pEPOcos6_ORF9 sequences:

(1) nucleotide sequence

Seq ID No 57 (>pEPOcos6_ORF9.seq)

ATGAAGTTGAACGTGGTCGCCAACCGGCTATTCGACCCCGAGTCGCCCGAGCGCACCGAGCCC
GCCAAGAGTCTGTTGCTCGCGGTGACCAAAGTCCTGCCGCAAGAGGTGCCCAACGTTCGAACC
CGCGCCATCAGCGTGGACCTGGATCGCTCGTTCGACGCGGCGGCGCCCGCCTGGGCCGCCAGT
TTGTTGGTTGAATGCGGCGCGCCCGTCGAGGAAACGGTGGTGACCTACCATGGCGCAGCCCGA
TGGCTGCGCCGCTTCGATCGCGTTGCGGTGAATGGTCTCGGCCCGTTCCACCCCGATCAACCT
GCGCCGCTGCTGCGCGAGCGCGGCGTGTACCTGATCACCGGCGGCCTGGGCGGCGTGGCTGGC
CAGTTGGCGCGCTACCTGGCGCGGCCTGCCGGGCGCGGTTGGTGCTCACCGCGCGCCGGCCC
CTGCCCGAGCGCGACCAGTGGGATCGGGAGTCGGCCGTGCTGTCATGGGACGACAAGACGCGC
CAGCGCATCGAGCTGGTGCGCGAGCTGGAGCGGCTGGGGGCCGAAGTATTGGTGGTGGCTGCC
GATGTCGCCGACGAAGCGGCCATGGCGCAGGCGATCGAGGCCTCACTGGCGCGATTCGACGCT
TTGGACGGCTTGATCCACGGCGCCGGGATCGTGCGGGTCGCGTCGGGCCGCACGCCGATCGGG
AGTATGACGCGGGCCATGTGCGAGGAGCAGCTCCGCCCCAAGATGTTGGGCCTCGACGTCGTC
GACCGCCTCCTGCGCGATCGCCGGTTGGACTTCCGCATTGCCATCTCGTCGCTCGCCCCGATT
CTCGGCGGCCTCGGCCACGTCGCCTACGCCGCCGCCAACCTCTACATGGACGCGTTCGCGACG
CGCGCCGCCGCCGGCAACGCGCCTTGGATCGCGCTGAACCTGGCCGAGTGGGAATACGAGGGC
CCGGCTACCTACGACGAGCGGGTGGCCGTTCGCTCAAGCAGCTCGAGCTCACCAACGAGGAG
GGTATCCGCGTCTTCCAGACGGTGTTGGCCTTGGCCGCGCGCGGCCCGCTACAGCAGATCATT
ATTTCCACCGGCGACCTCCAGGCCCGCCTCGACAAATGGATTCACATCAAATCCCTGCATCGC
CGACCGGGGCCGGTCCAGCTCAGTCGCCGGACCGCGGCACCCCAGGGCGGTTTCGGCTCGGAG
CGCGCCGCCTTCGAGGCCGCCTTCGCTGACGCCTGGTGCGACTTCTTCGGGGTTGAAGAGGTC
GACCCGAACAAAAACTTCTTCGATCTGGGCGCCAGCTCGCTCGACTTCATCCACCTCGTCAGT
CGCTTCAGCAAGGCCATCGAACAGCATGTACCGCTCGAGGCCCTGCTCGAACACTCCACCCTG
CACGACCTCGCCGCCCACCTCGCGGGCGACGCGAACACCGACGCCAGCGACGAAGCGCGCATT
CGCCAACGGCTGCAAGGCGCCAAGTCCGGCGACATCGCCATCATCGGCATGGCCGGCCGCTTC
CCGCTCGCGCCCGACCTGGACACCTATTGGCGCAACCTGGTCGGAGGCATCGACGCGGTCAGC
TTCTTCAGCGCCGAGGAGTTGCGTGCTGCTGGCGTCACCGCGGCCGAGATCCACCACACCAAC

TACGTGCCGGCCAAGGGGCGCTGCGCCGACCAGGACTTGTTCGATGCGGCCTTCTTCGAATAC
ACTGCCAGCGACGCCGAGCTGATGGACCCGCAAAATCGCGTGTTACACGAGGTCGTGTGGCAC
GCGCTGGAAGACGCCTGTTTCGACTTCAACGGCGATCACGGCCAGGTCGGCCTGTTCGCGGGC
GCCTCGCCGAACCTGTGGTGGCAGTTCGTGGCCAGCTTTTCCGAGGCCGCCAAGACGCAGGGC
ATGTTCACCACCACCCTGCTCAACGACAAGGACTCGATCGCGACCCAGATTTCATACAAGCTC
GGTCTAAAGGGCCCCGCGGTCACCTTGTTCACCGGCTGTTCCACCTCGCTGGTAGCCGTTGAC
GCCGCCTGCCGCTCGATCTGGTCCGGTCAATCGGACATGGCCGTGGCCGGCGCGGTCTCGCTG
ACTCTCCCCGATAAGGCCGGCTACATCTACGAAAAGGGCATGCTCTTCTCGGCCGACGGCCAT
TGCCGGGCTTTCGACGCCAACGCCACCGGCATGGTCTTCGGCGACGGCGCCGGCGCGATCGTG
CTCAAGCCGTTGGACGCGGCCCTGCGCGACGGCGACCCGATCCATGCGGTGATCAAGGGCTGC
GCCACCAACAACGACGGCGACCGCAAAGCCGGCTACACGAGCGTCAGCGCCCAAGGCCAGGCC
GAGGTGATCCGCTCGGCCCAGATCCTGGCCGACGTGGCGCCCGAATCCATCAGCTACGTGGAA
GCCCACGGTACCGGCACCAAGTTGGGCGACTCGATCGAGATCAAGGCGTTGAAGCAAGCCTTC
GCCAGCGACAAGAACGGATTTTGCGGCATCGGGTCGGTCAAGACCAACCTCGGTCACCTGATG
GCGGCGGCGGGGATGGCCGGCCTGATCAAGACGGTTCTGGCGATGAAGCACCGCCAATTGCCG
CCATCGCTGCACTGCGACGAAGTGAACCCCGACCTGGAGTTGGAGCGCAGTCCGTTCTACATC
AACACCCGCCTGCGCGACTGGGTTGCACCGGGCGGGCCGCTGCGGGCCGGCGTGAGTTCGTTC
GGGATCGGCGGAACCAACGCTCACGTCATCCTGGAGGAGCCGCCGACGCGCGAGAGCGGCACG
CGCATGCGCCACTGGAAATTATTGATGCTGTCGGCGGCCAGCGAGGCGGCGCTCGACCGCCAG
GCCGATAACCTGGCCGACTACCTGGAGCGCCATCCCGAGGCCCACCTCAGCGACGTGGCCTAT
TCCCTCCAGACCGGCCGGCGCGTTCTGGCCTGGCGGCGCACGGTCCTATGCGAGTACCGCGAG
GACGCGGTGACCAGTCTGCGCGAGCGACAGGCCAAGCGCGTCCAGACAAGTCGCGTCCGCTGG
GACCACAAGGACGTGGTCTTCATGTTTCCCGGTCAGGGCGCCCAGTACCTCAACATGGGCCGC
GACTTATACGTCATGGAGCCGGTCTTCCGCGAGGTCATGGACCGCTGCTTCGAGTTGCTGGCC
CCTTTGTGGTCCGAGCATCCGCGCCAGATCCTTTATCCGGAGGGCGGGGTGTCGACCCTGCTC
CACCGGACTGATTACACCCAGCCGATCGTGTTCTGCTTCGAGTACGCCCTCGCCCATTTGCTG
CTCTCCTGGGGATTGAAGCCGGCCGCGACCATCGGCTACAGCTTCGGCGAGTACGTTTCTGCC
TGCCTCGCCGGCGTCTTCTCCCTGGAAGATGCGATCCGTCTGGTGACCGAGCGCGGTCGGCTG
ATGGCGGCTTTGCCCGCGGGCGCCATGCTCAGCGTCCCGGTTCCCGAATGCGAGCTGCTGCGG
CTGCTGGACGGCTTCCACGCCCAATCGGCGGCCCATCTGGCGCTGGCCGTCGACAATGGCGCC

TCCTGCATTGTGGCCGGCGAGCAGGCCGCCATCTCGGCCTTCGAATCGATGCTTCGCAAGAAG
CGTCTGTTGACCATGCGGGTCGCGGTCAGCCACGCCGCTCATTCGCAGGTCATGACCGGCGCG
ACCGACGCCCTGCGCAGCATCCTGCGGAAGATCCCCCTCTCCGCGCCGACAATTCCCTTCATT
TCCTGCGTCACCGGCACCTGGATCACTGCACAGCAGGCTACGGATCGCGAGTATTGGGTGAAC
CACATGTGCGGGACGGTGCGGTTCGCGGCGGGTCTGACCGAGCTGGGTCAAAACCGCGAGGCG
GTGTTCCTGGAAGTAGGTCCGGGCCGCGACTTGACGTTGCTGGCCCACCGCATCCTGGCCGAC
AGCGCGGCCGTGTTCGAGCTGGTCAAGGCGCCCGACGGCGGCGACGACGATGGGTTCCTCCTG
CTGGATCGATTGGCCAAGCTCTGGAGGCTGGGGATTTCGATTGACTGGGCCGGCTTCTACGCG
GATGAGCGGCGGCGGAAACTCTCGCTGCCGGGATATCCGTTCGAGCGGCGGCGCTTCTGGATC
GAGGGCAACCCGCTGGAGATCGCCGCCGGCAGGCCCAATGTCCAGGGGCCGCTGGTCAAGGCG
TCGGACATCGGCGCTTGGTTCTACGTGCCGCAATGGCGGCGGTCGGTGCTCGCCGAGCCGGGT
ACAACGGCGGCGGGCGCCGCCGTCACGGCGGAGCAGGCACGCGTCGTGACCGAGCTACGGGCG
GGATGCGCGTCGGCCGGCTTGGGCAGCGGGGCCTGCGGACTGAATGGCGGTGCCCCGTCCGAG
CGTCCGAAAGAAAGTGTAGCGCCAGCCGGGTCGACCAGCGCAGCGGCGCAGACCGGCGCGGAC
TGCCCGACACCGACTGGGGAGCCAGCGGCTGTGCCAAAGGACGGGGCCGAGCCGCGGCCGACC
TGGCTTATTTTCGCCGACGCCGGCGGATTGGCCGAATCTTTCGCCAAGCGGGTTCAGGCCCGC
GGCGAGAAGCTTTACCTGGTGGCTTCCGGCTCGCGCTTCGAGCGCCTGGCCGAGACCCGCTTC
CGCCTCGATCCCGGGGCCAAGTCCGATCACCGCCTGCTTTTCAAGGCGCTCGACGAGGCCGAC
ATCCTGCCGACCCACCTCCTCGACTTCCGCTCGCTTGACTGCGGCGGGCCCGACGCCGACCCC
ATGGACCAGGCCGGCTTCTTCGGGCTGTTGCACCTGGTCCAGGCGATGGCAGAGGCCGGCTAC
AGCCATCCCATTCGGCTGCTGATCGTCAGTTGCGGCGTCTACGATGTCACCGGTGCCGAACCG
CTGCAGCCGGCGCGGGCCACGATGATCGGACCGGCTCTGTGCATCCCGCAACAGTATCCGCAC
CTCGAAACGAGCCATGTGGATTTGGGCGTGGTCCATGCCGACGAGCTCCACGCCGCGCGCCAG
CTCGACAGCCTACTTGCCGAATGCCTAAGTGCAACGGCCGAGCGCCAATTGGCGCTGCGCGGC
CGACACCGCTGGCTGCTGGACTACGAGCCAGTCCGCTTGCCGCCGCTCGACCCGGGCCGTCTG
CCCTGGCGCCAGCGCGGGGTCTACTTGATCACCGGCGGTTTGGGCGGGATCGGCCGCATCCTG
GCCGAACACCTGGCCCGCACGACCTCGGCTCGCCTGGTCCTAATCGGCCGCGAAACCCTGCCC
GACCGCGACGACTGGGACGCCTGGCTGAACCGCCCGCAACCGGTCGACGCCACCCACGAACGG
CTGCTGCACAAGATCCGCGCGATTCGCGATCTGGAAGCGCTAGGCGCCGAAGTCCTGGTCCTC
GCCGCCGACGTCGCCAACGAAGCCGCCATGCGCGAGGCCTACGATCGCGCCGAATCCCACTTC

GGCACAATCCACGGGGTGATTCACGGCGCCGGCCTGATGGACGCGCAAAGCTTCTCACTGATC
GACGCCCTCGACCACGACCTCTGCGCCCGCCAGTTCGAAGCAAAAATCCGCGGCGTCTGCGTG
CTCGACCGCGTTCTGGCCGACCGCACGCTCGACTTCTGTCTGCTGATGTCTTCCATCTCCACC
GTGCTCGGCGGCCTGGGCTATTTCGGTTACGCCGCGGCCAACGCCTTCCTCGACGCCTTCGCC
CAGGCGCGCAGCCGCGACGCCGCTTTCCCCTGGCTTAGCGTGGCCTGGAGCGATTGGAAGTAC
TGGACCGAGCGCAAGATGGACAACGAGGTCGGCGCCGTCATCGACAGCCTCTCGATGGAACCC
GCCGAGGGCTTCGAAGCCGTCACCCGCGTCTTGGCTTGGGGCAAGGCGCCCCACATCGCCAAC
TCGCCCGGTGACCTCGGTCGCCGCCGGGATCAATGGGTCAAACTGGCCAGCCTGAAATCGGCG
CACTCCAGCGAGCCCGAGCCGGCTAGGCATGGACGTCCGGCGCTCTCCAGCGAATGGGTCGCG
CCGCGCAACGTGGTCGAAGAGAAGCTGGTCGCCATTTTCGAGCAGGTGTTCGGCACTGCGGCA
CTGGGCATCGAGGACAACTTCTTTGAGTTGCGCGGCGACTCGCTCAAGGCGGTCATGACCGCG
GCCCGTATTCAAAAGGAGCTGAACGTGGAAGTGCCGCTGCCGACCTTCTTCCAGATGCCCACG
GTCGCTGGCCTGGCCCAGTTCGTGACGCAAGCCAAGCGCAGCGGCCGGGAGACGATTCGGCGC
ACCGCGCCGCGCCCACATTACCCGCTCTCGGCTGCCCAGGGCCGCCATTACCTGCACTACCGC
ATGGACCCGCGTTGTACCGCATACAACGATCCCTTCGCCAACCTGATCGAGGGTCCGCTGGAC
GTGGATCGCGTGGAGCGCATCCTGCACACCCTCATCCTACGCCACGACTGCTTCCGCACCTCG
TTCCACTTCCGCGAGGGCGAGCCGGTCCAGGTGATTCACGATCGGGTGGACTTCAACCTGGCG
CGGATTACCTGCGCGCCCGAGGATTTGCCCGAACGGATGCGCGATTTCATCCGCTCCTTCGAT
CTGGAGCGACCGCCCGCCATGCGCGCCGGCCTCTTCGTCACGGGGCCCGAGCGCCACGTGCTG
CTAATCGATTTTCACCACATTATCACCGATGGCGTGTCGTTCGAGAACTTCGTCGGCGAGTTC
GCGGCGCTCTACCGCGGCGAGATCCTGCCCGAGCTGGAACTCGAGTACAAGGATTTCGCGGTG
TGGCAGCATGAGAACCGGGGCCGCCGCGCCAACAGCGACCAGGCCCGCTACTGGACCGAGCAG
TTGGCCAATGCGCCCGGGCCGATCGAGCTAACCACCGATTTCCCCCGTCCCAGTCGACGCAGC
TTCCGCGGCGACCGCGTGCGGACCGTGCTTGATGCGGAGCTCGTTGCTCGACTCAAAGAGCAC
GCGGCGCGCCTCGGCATCACCCTCTATAGCCTGCTGCTGGGCGGATTCTCGTTATTGCAGCAC
AAGCTCTCCGACTCGCACGACATCGTCATCGGTTCGCCCGTCGCGGGCCGCACCCGGAGCGAA
CTCCAGGATCTGCTGGGCGCGTTCGTCAACACCCTGCCGATGCGCCACCGCATCGACCCGACC
CATACCGCACGGGTCTTCTTGGAGCAGGTCCACCAGACAACCTTGGCGGCCCTCAGCTACCAG
GAGCACCCTTTTGACGAAATGGTGGCGACGCTCGGGTTCGCCGCCGATCCGGCTCGCAACCCG
ATCTTCGACACGATGTTCTTGCTGCAGAACATGGCCATGGGTGCAACCACCATTCCCGGTCTG

CGGCTCTCGCCTCACGACACTTTTCACCGCAAGGCATTGTGCGACCTGATGCTACAGGCGACC
GAGTATGACTGCCACCTGGAGCTGGTGCTCGAGTTCGCCACCGACCTGTTCCGGCTGGAAACC
GCGCAAGTCTTGCTCGACCGCTACCGCCAAGTCTTGGAGTGGCTGTTGGCGTACCCCCATGAA
TCGATAGACGATTTGACGCTCGCCGGCCACTTTCGCGAAGTCGAAGTGACGATGTCGGACGAG
GGCGACTTTGATTTCTCAGATTTCGAACCCCGCAACGTGAGAAACCTATGGCGCGCC

(2) peptide sequence

Seq ID No 58 (>pEPOcos6_ORF9.pep)

MKLNVVANRLFDPESPERTEPAKSLLLAVTKVLPQEVPNVRTRAISVDLDRSFDAAAPAWAAS
LLVECGAPVEETVVTYHGAARWLRRFDRVAVNGLGPFHPDQPAPLLRERGVYLITGGLGGVAG
QLARYLARACRARLVLTARRPLPERDQWDRESAVLSWDDKTRQRIELVRELERLGAEVLVVAA
DVADEAAMAQAIEASLARFDALDGLIHGAGIVRVASGRTPIGSMTRAMCEEQLRPKMLGLDVV
DRLLRDRRLDFRIAISSLAPILGGLGHVAYAAANLYMDAFATRAAAGNAPWIALNLAEWEYEG
PATYDERVGRSLKQLELTNEEGIRVFQTVLALAARGPLQQIIISTGDLQARLDKWIHIKSLHR
RPGPVQLSRRTAAPQGGFGSERAAFEAAFADAWCDFFGVEEVDPNKNFFDLGASSLDFIHLVS
RFSKAIEQHVPLEALLEHSTLHDLAAHLAGDANTDASDEARIRQRLQGAKSGDIAIIGMAGRF
PLAPDLDTYWRNLVGGIDAVSFFSAEELRAAGVTAAEIHHTNYVPAKGRCADQDLFDAAFFEY
TASDAELMDPQNRVLHEVVWHALEDACFDFNGDHGQVGLFAGASPNLWWQFVASFSEAAKTQG
MFTTTLLNDKDSIATQISYKLGLKGPAVTLFTGCSTSLVAVDAACRSIWSGQSDMAVAGAVSL
TLPDKAGYIYEKGMLFSADGHCRAFDANATGMVFGDGAGAIVLKPLDAALRDGDPIHAVIKGC
ATNNDGDRKAGYTSVSAQGQAEVIRSAQILADVAPESISYVEAHGTGTKLGDSIEIKALKQAF
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LDRLAKLWRLGISIDWAGFYADERRRKLSLPGYPFERRRFWIEGNPLEIAAGRPNVQGPLVKA

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pEPOcos6_ORF10 sequences:

(1) nucleotide sequence

Seq ID No 59 (>pEPOcos6_ORF10.seq)

ATGGCGCGCCTGAGCCGCACAGATCTCCAACTCGCCATTCACCAGCGCACCGTGGAGCGCGAA
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CTGAGTAATCGTTCGCCGCAACGCCTGCTCACGGTGTTGGCGGCTGGCCTCGCGGCTTTCCTC
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CGCGATCTGCTCTATGCGCTTCGATCCGAATACCACGAGGCGATGCGCCACGCCAACTTTCCG
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(2) peptide sequence

Seq ID No 60 (>pEPOcos6_ORF10.pep)

MARLSRTDLQLAIHQRTVEREYWRALFERHPQRSSLPGVLTAPIGDESTRETLSFVLDEDPLR
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VYLEVMRRHHAPPVPDRLRYVFVSGEALEPDHLAGLQQIGRRLGRTIPLVNLYGPTEASIEVS
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FVPNPFGNGERMYHSGDLALVRGDGQVAFLGRRDHQIKIRGQRVELGEIESHLRGLEGIAAAV
VQAESQHHETLLHAYVVTNDAGLNAARLRAALAQHLPEYMIPQRFSRLAELPLLAAGKIDRAA
LAQRATPLASGAPFVEPSGPTQQRIAELWRQVLAVAEVGAEDPFFSIGGNSLNVLKLSAALSD
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pEPOcos6_ORF11 sequences:

(1) nucleotide sequence

Seq ID No 61 (>pEPOcos6_ORF11.seq)

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(2) **peptide sequence**

Seq ID No 62 (>pEPOcos6_ORF11.pep)

MTNHDHHEESSGLEIAVISMACRFPGAADCDAFWENLINGTSSITHFSDDELIAAGVDARDLT
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pEPOcos6_ORF12 sequences:

(1) nucleotide sequence

Seq ID No 63 (>pEPOcos6_ORF12.seq)

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AACGTGGGCCACCTGAACGCCGCGGCCGGCGTGGCTGGTCTGGTAAAAACCGTGCTGGCGCTC
CAACACCGCCGCCTGCCGACCAGCCTGTTCTACCAGTCGCCCAATCCACACATCGACTTTGCG
GCGAGTCCGTTCCGCGTGAACGGCCAGACTTCGGATTGGGTCGCGCCAGAGGGGACGCGGTTG
CTGGCGGGAGTGAGTTCGTTCGGTATCGGGGGAACCAACGCCCACCTGATCGTCGAGGAGGCG
CCGAAAGCGCTACCGACGACAGCGGCACCTCTGTCGACGGAGCCGAATGACCTCGACGCGGGC
GACGCCGACGGGCTAGTGCTGCCGATCTCGGCCCGCACGCCGACCGCCCTGGCGCACATCGCG
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CTTCAGCTGGGCCGTCGCCAATGGCCCCATCGCCACAGCCTGATCTGCCGGAATCGAACGGAG
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TGCTTGGCCGGGCTTTTCTCGCTGAGCGATGCCCTGCTGCTGGTGAGTGAACGCGGCCGCCTG
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CGCCTGGAGCTTCTGGCCGACGACCGAATCAGCATCGCGGCGGTCAACACCGCCGAGAGCTGC
GTCATCGCGGGACCCAGCGAGGCGATCGAGCGCTGCGCCCAGCGCTGGGCCGCGCAAGGCCTG
ACCTGTACGCCGCTGCGCACGTCCCACGCCTTCCACTCCGCGATGATGGAGCCGATTGTCGAA
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(2) peptide sequence

Seq ID No 64 (>pEPOcos6_ORF12.pep)

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IREPLQALIVGPCLVIPQEFPGLSVRLLDVNVDDPAPRLAERLVAELSGTDHMVALRGGERLV
ADVDQVDGLGVGIAKVPLRREGHYLILGGLGDIGYHCARYLAQTYRAKLTLTARSSLPPRASW
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AANAYMDSFARRHDRPDECRWIAVNWDAWLFEAKTSSVGAELARLAIVPEDAPALFARVLERL
PQSFIVSTADLRARIDTWIRDKNRVPPAEIRAVQPRPDLSQAYAPPIGPLEIQLCGLVSAYCR

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pEPOcos6_ORF13 sequences:

(1) nucleotide sequence

Seq ID No 65 (>pEPOcos6_ORF13.seq)

ATGAAATACGAAACCACCGGATTGGAATTGGCCGTCATCGGTCTCGCTTGCCGCTTTCCAGGC
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AAAGGCGCGCTGGACCACGCCGATTTCGAACCAGCCTTCTTCGGCTACTCGCCCAAAGAGGCC
GAGGTGATGGACCCTCAATTCCGGCTGCTCCATGAGTGCTGCTGGGAGGCGCTGGAGTCAGGC
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CCGCTGTTCCGCGCGGAGCTGTTGCAGTTGGCCGAGCAGCGCCATCTGCTACTTTTCGACATG
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(2) peptide sequence

Seq ID No 66 (>pEPOcos6_ORF13.pep)

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pEPOcos6_ORF13.1 sequences:

(1) nucleotide sequence

Seq ID No 67 (>pEPOcos6_ORF13.1.seq)

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GCTGCTCCGCGCCCCGGTGAAGCGGAAGTGGCTGCCCCCGGCGCCCGTCCTGCGCCTGAGCGA
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(2)peptide sequence

Seq ID No 68 (>pEPOcos6_ORF13.1.pep)

MTQASAASTSQVAPEVTPGRKDDDDDQIRDVGRCSLCGERLPRWATRGRRDEAGPDAGAGRRE
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pEPOcos6_ORF14 sequences:

(1) nucleotide sequence

Seq ID No 69 (>pEPOcos6_ORF14.seq)

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GCCACGCCGCCCGATCTCGTCGCCCTCGTCCACCGGGTTCTGGCGTTCGATCCCGATGCGCGG
CCGCGCATGGCGGAGGTGGCGAGCGCGCTTCACCGGCTCGGCCGGGCGAAGAAGGAGCTCGAC
GAGGCGCTCTCGAGGTGGGTCGTCGGCGGAGGGGCGCCGGGGCTCTTGCCGTGCGGCTATGCT
CTTCTCGAACTGGTCCTCCTGGGCCCTGGGAACTTATACGATTCTTTCCAGCCTGTAAGTGCA
TTTTTCTTTCAATATCGTCCTCTCTTCATATACGAGGTGAGTTCTCTGAGGTCCTCCTATAAG
TCTGGGGTGTCCTATTCGGCCTCTTACTTGTTACTTCGCCTTCTTAGGAGTTTTTCCTTAATT
TTGCCCTCTTACATTCCCGTATTCATTCTAACTGGGCCCTATCTCATTCGC

(2)peptide sequence

Seq ID No 70 (>pEPOcos6_ORF14.pep)

MVTRPTSDGIEDELAPFPPVLRGWLIEGELGRGGMGRVFRARHPKTRARAAIKVLLGDYARRP
DVVARFRQEAIAVNIINHPGIVRVFDSGELEDGSPYIVMEYLDGRGLRDWVQAVPPAERPRQV
VRLGYQIASAMAAAHASKVVHRDLKPENIMVVEDELAPGGSRVKILDFGIAKVLWGGLPEVLE
LEGRGSLAPASASTIRTELSTRPAPTVGATTGPESPLGASATPESALGASATPESALGASATP
ESEAHEEDALRSLPVVTSGRPAIHPAPVEIPPEAVSSAASRGSRASIEPGAPAPQSEGAGQPT
MPFTQEGVWGLGTRSYMAPEQERHSGSVDVKADVYSLGVILYELLEGRTPDAPSAAWPPPMSA
ATPPDLVALVHRVLAFDPDARPRMAEVASALHRLGRAKKELDEALSRWVVGGGAPGLLPCGYA
LLELVLLGPGNLYDSFQPVSAFFFQYRPLFIYEVSSLRSSYKSGVSYSASYLLLRLLRSFSLI
LPSYIPVFILTGPYLIR,

or DNA sequences complementary to said open reading frames,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA sequences according to (a) encoding proteins or to fragments of said DNA sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products.

10. DNA sequence according to any of claims 1 to 5, wherein the DNA is selected from the group consisting of

(a) the following DNA Sequence:

Seq ID No 71 (>Contig43)

CGGGTATTTGTGATATGTGGGCNGTAGTCGTATGCTTCATTAAGTACATC
CGTCCGTNGTAGAGAGTGACTCTGTCGCAGCGATAATAGACACGCTTGTG
ATGCTATAGGGAACATAGAGTCNTAGTAGATGATACGACGAGATATTNGT
ATAGAGCGTATAGACCGACGTGTGAGCGTCATAAGTGTTGTGTGTCATGA
GTGTGCTCAGAGGACGTGCAGACATTATATGAGCAGATGATGAGAGAGAA
TCAATGCTGCAAGNTATTCGTCGAATCTACATTATATCGAATCGTGTATG
TGCGTTTGTCGCAGCGCGATNCGATGAGATACCGAAAGGGTATGTATCTA
TNTTCGTGACGCTCGATNAGAGCAAATCCGCTACCGTGGAGATATCGTGT
ATCGACTCCATCACGATCAGTATCATGATACGTCAAACGAGTACACTCAT
TATTGATAACACACGTANGTGTGCATGCACAGTTATCGAGTGTATTGTGT
GCATGAGAGGTATAGGATNTATAGGCGAGCATATATATCTATATATATAG
GTTAAGAGTAGAANACTATGAAGATGCAGGAAGTAGTATCTCGCGGACAA
ACGGNGTACCTAGCGGGGTTGAAGTATTATCGACAGTGTATAACGACTCA
ACAGGGNTACGAGGTACATTGTATTTACAGTGGTTGGAAGGATTGCGCGA
GGAAAGGTAGTGGTACCGTGTGAGCTACGATGCTCGGGATAATGGTGATT
AGATAGAACCTTAGCGTTGCTAGATGAGTGAGTGGTGGTATGAGTAGAGT
TTTTGTTCTAGCTTTGTGTCCAGCGAGGATTCGTTCAGTCTGAAGGGTAA
GAGTACGTCCATCGCACACCCGACCGTTTTGAGGAGTTCTCGGTGCGTGG
TCAGTGGGGTTTGGAGAAGACAGAGTTGATTCATAGGGTTATCAAACGAG
TTATGTGGATAGATGGTAGTGACCCCATTTGAGTGAGAGTGTTGGCGTTA
ACANCAGCAGGATNTAT

SEQ ID No 72 (>Contig44)

TAGGTCTTTGACACCATGGGAGCTGCTACCGATGTTGCCGAGCACGATCG
CGCCGGCGCCGACGAGCGACTGCAAGCCGGCCGCGGCCATTTACGCCTGA
CGAGCGAGGTGGGCGAAGTGCTGGTGCGCGCCGTGCGTGTCGAGCGCGCC
CAGGTCCGCCGTTGCGCCGTCGCCGAGCAGTAGCGCGCCGTCGAAGACGA

TCACCGCGATCGAGGTCAGCGTCGTGGGGGCGAGGCCGAGGAGCGCGAGG
ATGCCGAGCACGACGCCGGCCGCGCCGTAGACGAGCTTGGCGCCCATGCC
GCCGCCGAGCTCGGTGCGCGTGTCCCACTCGACGGGCGGCGCGGTGCGGC
TCAACGCGCCGAAGCGCGAGGCGATCGCGCCGCCCTGCGCGATCAGCGCG
GCGCCGAATACGATCGTGGCGATCTGAGGTGAGCTCTACTGGCATGATCC
CCGTCAGCCCGAGGATGGTGAGGACAATCGTCGCGGCGCCGCACAGTACC
TCGCACGAGCGAGCCTCCGAGCACGACCTTCGGCGTCGTCTCGTCCTTTG
GTCTGCGTCGCGCGCCCGAGTGCGGCGTTATGTGGCTCTCCGGCTGTGCA
AACCGTTCACGTTCTTCCGGTCCTGGAGTCAGCATCGGCATGATTCCCCC
GTCCTGCGGTGAGGCCTTGTCGCGCTCACGCGCGCTCCGACTTGCACGTG
CTGTGCCGGGTTCTCTCGCTCAGGAGGCGCCTCTCTTGGTGGTGCTTGCG
TCCTGGTCCGTTTGCCCGCCTGTGCGGTAGGTTTCTTGAACCAGGTGACC
TTCAGGGACCCCTTGATGCGCTCCATCGTGTCCTATGTCGATCCTTCTCT
GACTTGTATGGGTCTCGAACCAACTACGCTTGATCAGGCCTTCGAAGGGT
CCTTTGGGAGATCGACTCTGGATCCATACCGGGAGCCCCTGTTCTGCCGC
TCTCTTAAGTTTCCCCTTCTGTATCCGTGTCGACCGGAAACGCTTTATCT
CTAATGCGCTCTAATTGCGTCTCTGCCACACGTGCGCTTCACTCTGGATC
TACTTCTTCTCCCTAGTCTTCTACCTCCGTACCCTTATTTGTTGGTTCTA
TTTATTTCTTTTCGCTTCACCTCGCGTCATTGTCGCCTAGTGTTCCTCCC
TCATATCGCCTTTGGTCTCCCTCGAGCGTACAGTCCTCTCTCTTCAGATG
CTTTCCGGCTCCTCTTCTGCTGGCCCCTTATCCTTTCTAATACTTC

SEQ ID No 73 (>Contig48)

ATGCGCCCAGGAACACCCCGGTGCGGCTGCCGTCGAGGGACTGGGGTGCG
ATGCCGGCGTCCTCGAGCCCTTCCCAGGTGACCTCCAGCAGCAGGCGTTG
CTGAGGATCGAGCGACCGCGCCTCCCGAGGCGAGGTGCCAAAGAACGCGG
CGTCGAAGCCGTCCACCGCCTCGGTGAGCAGTCCGGCCCAGCGCGGCACC
TCCTCGCTGGGATGGACGCCGACCAGCGCCCAGCGCCGGTCGAGCGGCTG
GACCGCGTCTCGGCCTGAGTCGAGCAGCTCCCAGAATGCCTCCGGAGTGT
CCGCTCCGCCGGGGAAGCGGCAGCCAATGCCTACGATGGCGATCGGCTCG

GTCCGCTCTTGCTCCAAAGACGCGTTCTTTTTCGCAAGCTTGTCCATGAG
CAGAAGGGCATGCTCAAGCTTCCCGGCATTCGTGGTCGCCATACTCCCTC
GGTCCCTTACTCACCAACGATCTGCGCGAGCTGCGCCAGCTTTTCGGCGA
GCAACGCGTCCTTCTGCTCGTCCGTCATGCCCCGCAGAGCCTCGAGATCT
GCGGCATCGTTCTCGAAGCTCTTCTCCCGCTCGGTGGCCGGAGCGTGGGT
CGCGCCGGCATTCGGAAACAGAATGTCTAGCAAGCTCCCGCTCAGAGCTG
CTACGTTAGGGTAGGTCCATAGCAGGGTCGCCGGCACGGTGATGCCGAGC
GCGGCCTCGATGCGGTTGCGGAGCTCCAGGCCTATCAGCGAGTCCATGCC
GAGATTGCTGAACGGCACGTGCCGCTCGATCCTCTCCGGCGGAAGGCGCA
GCCCCCGCCCCAACAGCTCGCTCAAGTGCTTCTCCAGAATCAACTGACGA
TCTTCGGGCCTGGCGCTCTGCAGCGCCTCGCGCAGGTTCGACGCGTTCGA
CGCGCCTCGGTCGGCGCGGTCACGCTCCTTCAGCAGCTCCGCCCACAGCG
CCAATCGGGCCGCGTTGGGATAGAACTC

SEQ ID No 74 (>Contig49)

ACCACCGCTTCACTCAGTATGTACTTTGTTATACTCGTCTTAGTACAATG
ATATAATACTCATGTGTATTCTTAATCTCGGGGAGANAAAATTGGAATAC
TGGACACCGTTGCCGCATGCNGACTCTAGAGATCCCCCTGCGACGGTATC
CCACGGCACCGGTATGGCCGGCGCGCGCTCCGGGGGTCAACGCCCCGTGG
TTGCCTTCACGACAACGCCGGTCGGCGGGGCGCCGTTCGATGCCGCGGG
CCCGCGCGCGGCGGCGCGTTATCCTGTGGAGCATCTGGAGGGCGCTCACG
CACCTGTCAGTCTAGTTCTGGCCCGCCCGGAAGGAGTCCGGGAGGCCGAA
GTTGAACCCGATGTAGAGCGCGATGAACGACGGGAGCACGCGCGCGGGGA
TGTGCAGCGCGGCGCCGATCGGCGTCGCGAACAGGACGAGCTCGCCCGGC
ATGCCGGGCACGACATACCCGAGCAGAAACACGATCGGCACCACGAGCGT
GAGCTCGAGCAGCGATATTTCATGACCGACCGCGCGGGCGGCGGCGCCCG
CCATGACGAACACGCAGATCAACGTGCCGTTGACGTTGAGCCAACCGCCG
AGTCCCACCACGAAGAGCCTGAGCTCCTGCGGCACCGCCGGATAACATTT
GCGGACGAGGTGCAGGTTGAGCGGCGTCGCCAGCGCCTCGCTGCACGAGG
CCCACAGCAGCGGATAGACCTTGAGCCAGTAGTTGACGAAATAGTCGCGC

AGCGAGAACTCCGGGGCGGCGGCCTTCATCCGCAGCAGGCTCGCCGCATG
GAAGACGAGGCAGGCAGCGCCGACGACCCCGGACACGAGCAGATAGGAGA
GCATGAGGTCTCCGGCGCCGAGCGAGGGCGCCCCCGCCGAGGCGCGCGCG
AGGTCCCCCCCGTGCACCTGCGCGGCGAGCTGCGCGGGCAGCCCGCGGAG
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CGCGGCGCGCGTACGGCCGCGAACGACGTCACGATGCCGGCGTAAAGGGC
GAGGAAGCACGGGCTCGAGATGACCAGGCCCGAGGCGCTATAGAGGGTGC
GCGCGGCCTCGAACGGCGCGCCCGTGCTGTGGCTGGGGAGCAGCGGCAGC
CCGAACACGAGCCATGTGACGACGACCCCGAACAGGCACGCTGCCAGACG
CTTGAGGGCGAGCCAGCCCATGATGTACGCGAGCAGCCGCCCCGGGCGCC
CTTGCCGGTGCAGGCTCACGAAGGTCGGCACGAGGACGACGAAGATGACG
ACCGGCGCCAGCGTGGTGTACCAATGCAGGAGACCGTCCATGGCGCGGGT
CGACCACCGCGTGACGCTGGTCTCTCTGTCTGACTCGATCATGGCCCATT
CGCCTAAAACTAATGATCCGTTCTCAAATTGGTCAAAAAAAAGTTCCCTT
AAGACTGTTTTACTCCGGAATATTAATATATTTCTGAGTGTGAGGTGATG
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CTTCTCTCTCTACAAGAGAGGTTATATATGGTCTCGAATATCTCGTCCGC
TCTTATATATATTCTCTTGTGATAATATATATCGAGTGTGGGTACTCAGC
TCTCTTGGTGTAATCTATAACTCGGCATCTCTCATAATACCTTATATATA
CACACTCTCTCGGTCATATCTCGCATAATAGATATATTTTATATGTTCCG
CGTTTTATCCGAGTGGGATACACTTTTTCTATATTTTCTTTGGTGTGACG
CGTGGCGTCGAGCCTTATTATTGATTTGGTAGTCACGATATTCTCTAGAT
GACATCATACAGATGCTCATAACTCGATAAACACAGGTCGTACACGACGA
GACTCTCACTCTCACTCTT

SEQ ID No 75 (>Contig50

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GGAGAATCGTTGCGCTCTAGCAGCATCTATAGGATCCCCGCTGCTCTTCT
TCATGCACCTCGTGGAGCAGAAGTTCATCAACGCCTTCGCGATCATCGTG

GCGGTGAGCTTCCTGGCGTTGCTCCTGTCGCTCGTCGTCGCCGACGTCGC
GACGCGGAACACGTTCCCGCCCGCGCCTTTGCCGGCGCTGAGCCCGCCGG
CGCCGGCGCTGATCCCGCCGGTGCCGGGCGGATCCGTTGGGCCGTCGCCG
GAGCCGCTGTCGGTCGGCCGGTGATCGGTTGTGCGGGCGCCGTGCCTCGG
GCTTACTACCCCCTCTCGCGGGTGGGGATATGGCCGTGGATGAGGGAGGC
GATGAAAATCGTGATCGCCACGTGCGCGTTGTTCTAGATCGTCCCAGGCT
GACCGTCGGGAGCGCCCAGCACGAGATGAAGAGCCACACCGCGAGGACCG
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ATGCAGAGCAGCCCGAGCACCCATGTGTTCGTCCGCTGCGCGTGGCTGTG
CGGCCAGATGACGGCCGAGATGAGGAGCCAGAACCCGAGGACGACGTTCA
CGATGCGCGCCATGAGATTGCCAGCTCGAACCATGCTCCCTCCCACCTCC
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CCGTCAATCGGCGAGCTCGTGAGCCATGGCGACAGCCCGCCGACCGCGCC
GGCGGGTCTCTGGCCTGCTGGTCGCCGTGCCGGCGGCGGCGATGGGCCTG
CCTCCGGTCGGGCCGCGCGGGCGCGCGGCGCTCCGCGCGAAGCTGGAGAC
GCGGGACATCGCTCCCTCGCCCCGCGCTCGGACGAGCGGCGCGAGCCACT
TCTCGACGGCCGAGCGGGCACTAAGCTTCCGTCATGAGGCTCGGCGCACG
GCTCACCACGCACACGTTCTCGGCCGGCGCCGCCGGCATCAGCTTCGTCG
TCCAGCCGATCCCGGGCTCGGACCAGCTGTTCGTCATTCCGATCCAGTAC
CTGCTCGCGGCGTCGCTCGCGAAGGAGCGAGGCGCGCCGCTCTCGAAGGC
GGCGTGGTCCCAGGTCCACCAGCTCATCTGGGGCGGCGGCGCGCTTCGCC
TCATGCTCGGCTTGACCCTAGGGCTGATCCCGCTGGCCGGCGCGTTCACG
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ATGTCTTGGACGCCATCACCTCCTTCTTCACCGGGCGAGCGCGGTAGGCG
AGCGGTCCCTGGGTCGAGCCCACCCTGCGGCTCTAGGAGCCGAAGGGCGA
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CCGGAGCGTATCGCGACCGCCGCCACCGCCGCCACGGCGAGCACGGTGAC
CGCGGCGGCCGCCGCGATGGCGACGCTCCGGGCCGTGTGCTCGGCCTCGC
CCTTGATGCCGCCCCACCTCGCCTTGACCGTGACCAGGTCGCGCGCGAGC

CGCTCCTTGCTGTGCTCGATCTGCTCGGCAGGCCCCGCGGGCGCCACGAA
ACCTGCGCCGGCGCTGACGTGACCTCGCTCGCTGAGGGGACTGGCGACCC
TCTCCGTGTCGAACCGGATTGCGCTGGATGGATCCATATGTCCCGCGCTG
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GCTCCTGACGGCGGGCACCGAATGTTCGCCAGACGGGCACAAGGCGCACG
CCGCGGACGGATCGGCCGCACTGGCACTCCAGAGCGCATCGACGGATGGC
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GCGAAGAAATCTATAGCGATGCGAGCAGAAGGATATGTCTATGGGGGGCA
GTCAGAAACTGGGGACAGTCAACGCACATATTCTCTCCAANTGCTAACGA
CAGCGTGCGCAGAGGAAGTATCCTACTAGTGTAAGAGGGACATTCGATGC
GACCGCATAAACATTCAGTCTACAACGCGTGAGAGGATGGAACACCCCGC
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NAATAGTAGATATAATTGTAATACTGAGCTACCGACAGAAAGATACACAC
GAGTGTACACACATCACACGCAGAGTGGTACCAAATTCACACCATGCGAG
CCACAATGTGACACGGAGGAGCACAGCATGGGCGCCACTATGGAGGAGAA
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GTGCACGTGATATCAAACTCTCTGATCAACCACACACTATATAAGGAGTA
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SEQ ID No 76 (>Contig51)

GATCCAGTTACGCCCCGCCGCCTCGGTCACGCCGGGGTTTTCGGCGTCGA
CCGGGGACGGTCGGGGCGACAACCGGGGGTTGTCGTCAGCGGTTCGCGTG
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GCTGCCGTACGAGCAGCCCGAGGCACCGCGCGAGCTCCTGCCGCTTCCGA
TGCGCGGCGGCCTGCTCGGCCTCGTGCTCCGCGATTCGGCGCTGGCGCCT
GCTCTCCTCGGCGCGTTCCTGCGTCCGCGCGAACAGCACCTCCTGCACCT
CCGCGAGTTCCTCGGCGGTAGCGACCCGCACGTGATCCGCACGTCCTCCG
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CCGCCGCAGGCCTCGGGTCCACTCGATCGCGCGTCGTCCGGCGAGGGCTT
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SEQ ID No 77 (>Contig52)
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SEQ ID No 78 (>Contig53)
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CGCGGGCGGGGCGCCGGTATCGCCGGACAGGAGTACACGCCGCCGTCGAC
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GTACATCCGGTCGTTGAGGGGCGTCGCGCCGGAGCCGGGCGCGCGGACGC
CGCTGCCCGAGGGCCCGCCCTTCCTGCGCTCCGGCCCGGAGCGCCCCGCC
CCGCTCAGCGGGGGCGCGCCGGTCGGCCCGATCGAGGGCGGCAAGCCCGG

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GGCCGAGAGGCCCGAGCCCCGACTACCTCCATGTTTACCGCGGGGTGACG
GAGTGGCTCACGACCACGGATCACAAGCGGATAGGTCTCATGTTCTACGC
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CGGCGCCAAGGACCTCGCGTTCCCCCGGATCAACCTCGCGAGCTTCTACA
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TCATGACGGCGGTCAACTTCATCGTGACCACGCACACGATGCGCGCCGAG
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SEQ ID No 80 (>Contig55)

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SEQ ID No 81 (>Contig56)

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TGGT,

or its complementary strand,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA-sequences according to (a) encoding proteins or to fragments of said DNA-sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products.

11. Peptide encoded by a DNA sequence according to claim 10 selected from the group consisting of

Seq ID No 83

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Seq ID No 84

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Seq ID No 85

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Seq ID No 87

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Seq ID No 88

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12. DNA sequence according to any of claims 1 to 5 wherein the DNA is selected from the group consisting of

(a) the following DNA sequences:

Seq ID No 89 (>Contig10)

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CAGAGCTCCTGCCGCCCGCGCTCGGCCCAGAGATCGGGGTACGCTTGC,

or their complementary strands,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA-sequences according to (a) encoding proteins or to fragments of said DNA-sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products.

13. Peptide encoded by a DNA sequence according to claim 12 selected from the group consisting of

Seq ID No 92

>Contig11_002 591 amino acids MW=63639 D pI=5.80 numambig=0
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Seq ID No 93

>Contig11_007 361 amino acids MW=38862 D pI=10.42 numambig=0
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Seq ID No 94

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Seq ID No 95

>Contig11_021 1213 amino acids MW=131017 D pI=12.40 numambig=0
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SVGREAPGRVRRRRRRRWRRAPRLRPEEAAGVHDPRGGRRPPGAAAERERQGGPRRPAGS
RRGRAARRGRRPADRDRAAHRLGARGGLAGRGRRRDRQPLRARLHLAAPRARAAPARRAH
RGARARRGRRGAGRVADRPVPVPDHRATGAAARRGDGQGRAGRRRGAARRGAPRRATPPG
ARIAMSEPIETEDGGSDIAIVGMAGRFPGAPSVDALWENVRRGVESIARFPESEREEPPV
GASAAPGAPVVCAGGLLDDIDRFDASYFGYSPREAQLMDPQQRLFLECAVAALEDAGCDP
ARFPGAIGVFGGCGSNTYLLQLLSHPDLAATVDPHALMLASEKDYLATRVSYKLDLHGPS
VVVQTACSTSLVAVHMACESLLGGQCDLALAGGVSIGIPQKRGYPYVPGSICSPDGRCRP
FDARAEGTVGGSGVGIVALKRLADALRDRNTVHAVIRGSAVNNDGGRKVGFMAPSVDGQA
AAISEAQSVAGVDPGSIGYVEAHGTATAIGDPIEVEALTQAFRRKTPRKAYCALGSIKAN

IGHLDAAAGVAGLIKAAHVVRSGEIPPCVHFEAPNPKLDLAASPFFVPREAAPWPRELRP
RRAGVSSFGIGGTNAHVVLEEPPPLPPRAPAPERDHVLTLSARTPEALSTACAQLAAHLE
ATDVPLDDVAFTLQTGRAEHPYRRAVVARTRAEAIQGLAREGASALARPDEPRPSSRSRA
RARRPSGWPARSTRRRRRSGAPSTRARRRRGRAASISARSSSARARATGARCSAPRWRSP
RSSPSSSRSPGSG*

Seq ID No 96

>Contig11_026 3079 amino acids MW=332984 D pI=5.97 numambig=0
MLTVVDHHVVVEYWSFALIVRELGELYSALRAGRPPQLPPPSSFFAAGVSCPSPREAAGG
AEYWRKALDGATTAIDLPRDRARHDAGARRGRAHAITLPKPLTGALARLARERGTTLFSV
LLSALTVLLHRASGQSDLVVGVPSAGRHDDESARAFGYFVQMLPVRVALRGAASFDALVA
RVRDAFLDALAHGDSALRHLLARAQGEAQRDALFDVAFAFQSTPPSLDARLSALAIGVGD
VRIAQGELELTTLADEQAAAEFDLALFAAELDAGIALRFEYDQQLFDPATIERMARHFVV
LLESAVEHPGRPLSELRMLSDAERALLLDDWSGAAAARQAASAPAPACVHALFEAHAARQ
PDATALEFGHQRFTYAQLSTWSTELALWLRDRGVGPGSVVGVCIERSPRMVAAQLAVLKA
GAAYASLDPANPPARLAEMLADCRASLALTSSQASHKLTAAPCPVHLVQDGACAPSTHIP
LVSRPDDLAYVLFTSGSTGTPKGVCVRHASLSRLVSFLHLRLDLSPSDRWTQVASSGFDA
SVYEIWTPLACGAALLLADDDALRSPTALVSWLVAQRATLSFMPTPLAEACFEQDWTGSA
LRAMTVGGDKLHPLRRPLPFRLFNMYGPTEATVITTVAEIADLGAEPPLGRPVDSALVYV
LDPHMQPVPPGALGELYIGGACLAQGYTRTDLTAERFLPDPFGQPGARLYRTGDLVRWRP
DGQLAFAGRRDEQVKLRGRRVELGEVESVLRRLPGVREGIVVLHGQGSAAHLIAHVVPDA
HPPSERDLREGMARLVPDALVPAHFVLLPALPMSLSGKVDKKLLPAPPAAHADYEPPSGE
LELELAHIWQSVLHLDRVGRHDSFFDLGGHSLLAMQVLGRIESSLGIRTTLRTLFEHPTL
AQLASHLSSGAASTSAAAATALERGLTRPDGPSSPRVATPEEPFALTEGQRAMWLECQKS
ADGALYNLGRTVRLGAGVDVAALRRAFEGLVERHEALRTTFLTRDGHPLQQVHRHVALEW
AEEPAMALDEREIVARADEVRRRAFDLERGPLLRVHVWRRGEGQPPLLTVVVHHLVVDYW
SFALLVRELGELYSALRAGRPPQLPPPSSFFAAGVSCPSPREAAGGAEYWRKALDGATTA
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QNDLVVGVPSAGRNDDESTRAFGYFVQMLPVRVALRGAASFDALVARVRDAFLDGLAHGD
SALQHLLAEPRGAARRGGALFDVAFAFQGALPSLDPRLAALTTGAEDVRIAQGELELTTL

ADEQAAAEFDLALFAAELDSGIALRFEYDQQLFDPATIERMARHFVLLLESAVEHPGRPL
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TYAELSTWSTELALWLRDRGVGPGSVVGVCIERSPRMVAAQLAVLKAGAAYASLDPANPP
ARLAEMLADCRAALVLTSSQASHKLTAAPCPVHLVQDGACAPSTHIPLVSRPDDLAYVLF
TSGSSGTPKGVCVRHASLSRLVSFFQHLLALSPRDRWTQLASSGFDASVYEIWTPLACGA
ALLLADDDALRSPTALVSWLVAQRATLSFMPTPLAEACFEQDWTGIALRAMTVGGDKLHP
LRRPLPFRLFNMYGPTEATVITTVAEVADLGDEPPLGRPIDSALVYVLDPHMQPVPPGVL
GELYIGGACLAQGYTRTDLTAERFLPDPFGQPGARLYRTGDLVRWRPDGQLAFAGRRDEQ
VKLRGRRVELGEVESALRRLPAVREGVVVLHGQGSAARLIAYVVPGADPPSERDLREGMA
RLVPDALVPAHFVLLPALPMSLSGKVDKKLLPAPPAAHADYEPPSGELERELAHIWQSVL
HLDRVGRHDSFFDLGGHSLLAMQVLGRIESSLGIRTTLRTLFEHPTLHQLADRLSSGAAS
TTAAAATVPASEIAPSLGRAPADEPYPLSYEQERLWVLEQLLPGGTAYNVVQAVRLRNLV
DVDALSSALAALVRRHWSLRTVFVASPTPAQKICEPEAAPAEVVDLRGTPPDEAEAAARA
WASREQATGFDLARGPVFRARLFRLDHDVCVLVLSTHHIVTDAWSFQPLVRDLAELYRRA
RGGGPADMPELPLQYVDFAVWQRRHLAGKRLADKLAHWTATLRGLPVLELQTDRPRPPVQ
TFRGAERVLPLDARLVAQLDELARSRGATRFMVLLAALGVLLRRSSGQDDLAIGTAVANR
PRPELEPLVGFFVNTIVMRLDLGGDPTFEELLSRARKVALEAFEHQDAPFEKVVEAVNPR
RDLSRSPLFQVMLVVQNAPTEALELGEVRIEPLDLPVEATRFDLRFSVEPRGGRDVISLQ
YNVDLFDAATIDRMLATMQSVLSRATQDPAQRVRALSVAPEDRERALVAWNDTAVATPDH
LRLEEPFFERAVEQPDACAVVDAERRLTYGELARRAEAIAAAASRSGATANALVAVVMEK
GWEQVAAVLGVLRAGAAYLPLDPRLPEERLRHLLEHAEVRLVLTQSAVDGTIAWPAGIER
LAVDADERWREQPVARRPPGGSTDDLAYVIYTSGSTGLPKGVMIDHRGAVNTVLDINRRF
DVGPEDRVLALSSLSFDLSVYDVFGTLAAGGAVVIPDRTRASDPGHWRELVERERVTVWN
SVPALMEMLMDASPGAGDPALSSLRLVMMSGDWIPLKLPDRIRAACRAPRVVSLGGATEA
SIWSIAHPIADVDPAWRSIPYGRPLANQHTYVLDEGLEPCPIGVPGEIHIGGIGVALGYW
RDEARTRERFLKHPTTGERLYRTGDLGRYFADGTIELLGRTDHQVKIRGFRIELGEIEAA
LAQHPSVEQAVVAAKTDPSGEKRLVAYVVGADGDGAALRDFVRKKLPEYMIPAEVVVLPA
LPLSANGKVDRAALPDPAAVAPRAAAVAPRTATERLIASVLAEVLQVEAVGVTDNLFELG
FTSLLLVRAQRLLAERIAARAPDEGAAAQAVSLTDLFQYPTIEQLAQRLDAATVKAEPAD
VGAQRAEARRDARRRRGRG*

Seq ID No 97

>Contig11_011 544 amino acids MW=60164 D pI=9.10 numambig=0
MMSRIRAQLGVELPLRALFQGPTVAALAAQVDAARRGEARRREFPPIARIPRDGPLPLSF
AQHRLWFVDQLEPGSPAYNIPFVVRATGRLDVDALRRSLFEIARRHEALRTTFSARDGVP
FPVVAPEARVPFRMSDLEHLAGEALDAAVSALVLEESLAPFDLSRGPLLRVRVIRKRHDE
HVIALVVHHVVFDVWSVGVFVGELAALYGGFAQGQPSRLPELPAQYVDFAAAQRAWLSGE
VLEGELRYWTTKLSGALRRARVPVDHEPAGRRTWRGARRSLDAGAELTRQIKAFCEREAI
SPFMALLAAYKLVLHQRTGLEDLVVGTDVANRNRVETEPMIGFFVNQLVLRTDCGGDPTF
GALVRRVRDVALEAFEHQDLPFDRLVEALRPKGAVGHVPLFDAKFVMRNVHVPPMKLEGL
ELEALEGEATTTAFDFVLTVAEAGGSFRFGVEHSSELYRAATVDNFLSDYRQILATATAR
PDTPVSELRGELERAAAARRELERKAARGAALDKLTSARRRAVTLPRPGAPGEAKTSPKD
DLDE*

Seq ID No 98

>Contig12_001 514 amino acids MW=56145 D pI=8.82 numambig=0
PPAVRRYVADRRPEQLPALAPEEREAAARRLSALGAAPPQVRRRGLTRAPLSYGQSRIYF
LEQLSPGKPLFNVPGAVRLRGPVDVARLSAAFGEIVRRHDALRTSIANVDGELLQIAQPH
AGFALDVVTSTPEEAAELDRRLRAEAWRPFAIGAPPLLRATLFRLAEDEHVLLVTMHHVV
SDDWSLGVILRELLALYAGRSLPPPRLQVSDFAAWQREMVESGALDGQRAYWRERLRGLS
RASISAGGGAEAPSHDPSGAIEEIALSPDKAAALEALARREGATLFMVLLALLDLVIHAR
SGALDIAVGTPIANRNRPELEDVVGLLTNTLVIRVDLARAGAFRDVLARARVQALDAFAN
QDIPFDVVTQDLKQERDHAQHPLFRVWLALQNAPKPALEVRGLRVEPLPLRPELVHFEVA
LLLWPADDGSVVGHFEFRRDRVDEGARKEIAAAFTHLVDAVIARPDAPVSTLVEGARAEA
ARAQAALGEAFARAATARLGQLRRRSAGDRTPRE*

Seq ID No 99

>Contig12_009 582 amino acids MW=65555 D pI=8.72 numambig=0
MREPSSTPNWRNFGSNLPAGSDSVPPGEGFPIKKILALNLGKWKDTAGLQIAQALHLFEY
GYKRYREGKFVLRATSDLGLGAIFESIDNWESFDQFEEFFKPWTFIRKPLVATRWAEDAE

FGRQRLVGINPAHIRRATPADLADFVSGAEPKPIAIADGRTLEEVREGGQLYFLDYRIFK
DIVDTDVQEELGKYPLAPTCMLHQTAAGELLPVAIRLVHSRPGKGAHPDKIFTPSGPSDD
WLTAKIAVASADAIYQGQVTHLLYAHLIVEPFAVSTYRNLPATHPLHQLLRPHFFNTLAI
NELARRRFLGRGRFFDITSSVATMGSFELLTRAYTGKGIKGYGGKPWRFYESALPRDLSA
RDVRDLVGYHYRDDALLHWDAIQEYVGQVLKIAYPTPGSLSSDASLQRWIHELVSPQLGG
MDSLLPPERADQLEKLTSLDDLIAIVTNIIFTATAYHAAVNFGQTDYYTWIPNAQFATYR
SYGDVLNGSEKRQFKPLERLPGRAQSIRQMVLSRSLSMGPPLTSESLMTMKCLLQDPAAK
QAFARYRERLAHIEREITERNRAREQPYLYLLPSMVPQSVAI*

SEQ ID No 100 (>ORF1)

VSQRTSCYLRGGGVCSMNDAFLALERNERNRPSTVIDLLRQRAEAEPARPIYCFLESGDVEAG
ATWVTLREIDERARTVAALLQASGVAPGARALLLYPPGIEYITAFFGCLYAGVRTVPAYPPDL
GRLERTLPRVASIVADARAEAALTSSAVAGIVASLPASAAAAALQRLRWIATDGPSPGPIEGP
GAALRPESVAFLQYTSGSTGEPKGVMLTHGNLLHNSRLIAHGFDLTSPDPVGVIWLPPYHDMG
LIGGILQALYRRIRVALMSPLSFLQRPMRWLRAVSALGASVSGGPNFAYDLCVRKSSEEERAA
LDLRSWEVAFTGAEPVRADTLDRFARAFAVSGFRREAFYPCYGLAEATLIVSGGARAEAPVLA
RLAPEEVELGRAVASAAEGARVFVGSGRALDPRAVAIVDPAGNELGPGEIGEIWVSGPSVAVG
YWGRPEETEATFGATLAGSAAPRYLRTGDLGFLRGGELFVVGRSKDLIILRGRNHFPQDIEKT
VESSHRAVRPGCSAAFSVEHEGEERLAVVCEVDPRVAADPREIVAAREAVTAEHQLVAHAVAL
IAPGALPKTSSGKVRRRECRRAFLEDALGERHVAFAPELLDDASPPDDAPPETEEPSGRSLLD
ALRSTLARALRLDAGQIDDALPISRFGLDSLAAVELQHAFQVRTGRAIPLTSILRGGSLRLTR
EITRLDGPSSPRVATPGGAVCADRWGTGRFGSSAISRPMERFTTWAGRSGSVPAFKRVDLRRA
F

SEQ ID No 101 (>ORF2)

VYSSAYVLFAVCAGTTRVASAPETAGFPLECVGDDGTVLGPDSFVVGYTQVYVFKKERLNTNP
PIDGFTLKLDGNEVAPGEDGLPVVKRCVRSEEQAQGCGRTEPAEDECTTYEIEAVVPEKAAEV
DEEAAGLGGPPAREAIWVDYYTDGGEFDGARRLVSDTTGASRGGNGTTWTPPSEPGRVSLWAV
VHDTRGGASVTRREVQVE

SEQ ID No 102 (>ORF3)

VVGTVLSAGTGEPLPDIAVTLVRPDGGREEAKTDQGGKFRFKNLPPGKYRVEVAAAGFEPFAA
EEEIAAGEAIEVRYRISLAAPQDGKAPGIEVTVQGERPPREVTRRTIERREIDRIPGTGGDAL
RSLQSLPGVARSGFGLLIVRGSAPQDTLTFVDRTPVPIIYHFGGLSSVVPTEMLEKIDFYPGN
FSAVYGRAMGGIVDVGLRSPKQDGKYHGVVQLDLIDGRVLLEGPVPFLKDWTFIAAGRRSWVD
AWLGPVLKEAGSSVTQAPVYYDYQFVLEGRPSASERVRASFYGSDDAFKITLDKPPEDEPALT
GDFGLHTAFQRFQLSYENRIGSRDRLLWSMALGRDIADFEISPLAFNVVSTSLDLRLELSHRF
ARYLTMNVGTDLSGGVATVNIRAPSQQPAGHPSNQPFSTYPFQDRSFDGAYSRPAAYAELEVV
PSPRARIVPGVRVDYALDTQTLDVSPRVNARYDIRSGFPRTTAKGGVGLYYQAPQFAESIEPF
GNAELKSNRAVHYGLGVEQEITPQIEVTLDGFYKQLDRLVVFSPEKDDYADGTGYAVGGELLL
KYKPDERFFGWAAYTLSRSVRKDGPDEEEHLTQFDQTHVLTVLGSLRLGRGWELARFRLVSGN
LQTPYVCDPEEKGCNPNRVNAIYHASSARYSPIPLGGDYSERMPLFHQLDIRADKTWKFKRWQ
LGLYLDIQNVYNYMAAEGISYNFNYTKREYVTGLPFLPTLGLRGDF

SEQ ID No 103 (>ORF4)

VIAVDNNPEAVDAVKDKTSAAFVGDATVHKVLEGIGAQYVETAIVTFGEHFEPSVLCVASLVR
MGVRIIARAATDRQADILRAVGATRVIQLETEMGRRVGADITMPLAQDLLDLASHYRVVPWNA
HGPLVGQTLAGSKIRQRYRINVLGVRPHTNKRPGDKPRLEAPTPDYVIRDGDTLLLVGDSDDV
SRFVAEVGG

SEQ ID No 104 (>ORF5)

SGSSGGGSSAEGSRCQPSGGGPHWLLEGETVTFPVTCASGLALAGDAFEVGPLPEGAAYDPIA
REVTFSPGLDQAAVYDIEIRVAQTSEVGRVKVGVADAFADPSNVPVVDPTRYPEEYGLPVLFL
SPVPEDKEYAPATVIYRGHTYAAEAELRGESSLSYPKRSYTLKFPKDDKFNEPDEAGGFTDRR
KVVLITTFDDNSYVRQRLAYDLWNRLDPEHIQIKTYSAVLYLDGEYAGLYTVADHVDGYLMED
HGYPQDGNLYKAVSHDANFALTDRSGDPKDTLHDGFEKKEGAPAEGEPEAFSDLEDLVSFVAE
SDDATFAAEIGSRIDLRDYEDWWIFVTFIVANDSAGKNSYHYRDPAADGVFRYAPWDFNASFG
QSWETEREPASDRVDYRDVNLLFERLLEEPSIGDPLRARYDQVLRGALAEAEIHAIVDGYVER
IDASARRDEARWGEAYRSYEGWSWRDDFTTYEEEIAYLK
AWISERWQHQDELY

SEQ ID No 105 (Contig 11 >ORF1)

VLDVWSTSDQVACRLHCAGAGPSASLELRYDASAGARRDAERLAERLAALLEDLSRHPERPVA
QGEVGPGERAEIEAWSRGPAMELPSACALHRWFEERAEQHPDVVAVRSEGKSLTYGELERRAN
RLASCLRRRGVGLDTIVGVCVPRSEDMVVATLAVLKVGGAYLPLDHEYPGERLAFMMRDARAR
LLVTHDAIADELPTGGWTTLLLDAEAAEIAACSDARPAVSPPPDSGAYVIYTSGSTGTPKGSL
ISHRAIVNQMQWIQRYWALTADDRVLLKAAFGFDVSVWEIFWPLSFGARIVVARAGGHRDPEY
LRRLVRDEGATTAYFVSSMLAAFLGGPEQPFPASLRKVLVGGEAVPLDLVRRFYAKHDGDLIN
MYGPSEAAIAVTGCVLPSDPRVTWVPLGAPVANAEVFVLDGAMRRPAIGALGDLYIAGAPLAR
GYVGQPGLTAERFLPDPCARAAGGRMYRTGDVARFLPDGMLEFQGRSDHQIKLRGHRIELGDV
EAQIRRVPGVGQAAVVLREDAPGDARLVAYVVLDGDAAGDAPDVRAGLKASLSAYMIPSSVVR
LYALPMCSERLAFTGSSYAGCLL

SEQ ID No 106 (Contig 11 >ORF2)

MSDHEMTGFSLSPQQRAIRALDREAGAPGCRTLAVVAVTGPCDEGRLSAAALALAERHEILRT
RLVEGRARPRRWSASRASRGRQQDDWVGCSEAEQGERMSRLVARLSEDRGADDGLRVGLVRVG
PEERRLVLAAPAWCVDEESIAPLVRELCASTAGAGAPPEQQYADVAEWLNGMLESEDAGDGRR
FWAERRSHFGPPLHLAFSRGGAGAGAGSGRARVDLQGGMAQVERWSSSWQVPQRIVLLALWAS
LLWRMSGGNEPEVTVAVRFDGRSLDALAGAVGPFARFLPVRIEISASDTLADVARRLALAEAE
AAAHQDAAPGVSHRMSWGLLRRGGRAGAVARRRAGPRARRLEHV

SEQ ID No 107 (Contig 11 >ORF3)

MSRIRAQLGVELPLRALFQGPTVAALAAQVDAARRGEARRREFPPIARIPRDGPLPLSFAQHR
LWFVDQLEPGSPAYNIPFVVRATGRLDVDALRRSLFEIARRHEALRTTFSARDGVPFPVVAPE
ARVPFRMSDLEHLAGEALDAAVSALVLEESLAPFDLSRGPLLRVRVIRKRHDEHVIALVVHHV
VFDVWSVGVFVGELAALYGGFAQGQPSRLPELPAQYVDFAAAQRAWLSGEVLEGELRYWTTKL
SGALRRARVPVDHEPAGRRTWRGARRSLDAGAELTRQIKAFCEREAISPFMALLAAYKLVLHQ
RTGLEDLVVGTDVANRNRVETEPMIGFFVNQLVLRTDCGGDPTFGALVRRVRDVALEAFEHQD
LPFDRLVEALRPKGAVGHVPLFDAKFVMRNVHVPPMKLEGLELEALEGEATTTAFDFVLTVAE

AGGSFRFGVEHSSELYRAATVDNFLSDYRQILATATARPDTPVSELRGELERAAAARRELERK
AARGAALDKLTSARRRAVTLPRPGAPGEAKTSPKDDLDE

SEQ ID No 108 (Contig 11 >ORF5)
MSEPIETEDGGSDIAIVGMAGRFPGAPSVDALWENVRRGVESIARFPESEREEPPVGASAAPG
APVVCAGGLLDDIDRFDASYFGYSPREAQLMDPQQRLFLECAVAALEDAGCDPARFPGAIGVF
GGCGSNTYLLQLLSHPDLAATVDPHALMLASEKDYLATRVSYKLDLHGPSVVVQTACSTSLVA
VHMACESLLGGQCDLALAGGVSIGIPQKRGYPYVPGSICSPDGRCRPFDARAEGTVGGSGVGI
VALKRLADALRDRNTVHAVIRGSAVNNDGGRKVGFMAPSVDGQAAAISEAQSVAGVDPGSIGY
VEAHGTATAIGDPIEVEALTQAFRRKTPRKAYCALGSIKANIGHLDAAAGVAGLIKAAHVVRS
GEIPPCVHFEAPNPKLDLAASPFFVPREAAPWPRELRPRRAGVSSFGIGGTNAHVVLEEPPPL
PPRAPAPERDHVLTLSARTPEALSTACAQLAAHLEATDVPLDDVAFTLQTGRAEHPYRRAVVA
RTRAEAIQGLAREGASALARPDEPRPSSRSRARARRPSGWPARSTRRRRSGAPSTRARRRRGR
AASISARSSSARARATGARCSAPRWRSPRSSPSSSRSPGSG

SEQ ID No 109 (Contig 11 >ORF6)
VVDHHVVVEYWSFALIVRELGELYSALRAGRPPQLPPPSSFFAAGVSCPSPREAAGGAEYWRK
ALDGTTAIDLPRDRARHDAGARRGRAHAITLPKPLTGALARLARERGTTLFSVLLSALTVLLH
RASGQSDLVVGVPSAGRHDDESARAFGYFVQMLPVRVALRGAASFDALVARVRDAFLDALAHG
DSALRHLLARAQGEAQRDALFDVAFAFQSTPPSLDARSALAIGVGDVRIAQGELELTTLADEQ
AAAEFDLALFAAELDAGIALRFEYDQQLFDPATIERMARHFVVLLESAVEHPGRPLSELRMLS
DAERALLLDDWSGAAAARQAASAPAPACVHALFEAHAARQPDATALEFGHQRFTYAQLSTWST
ELALWLRDRGVGPGSVVGVCIERSPRMVAAQLAVLKAGAAYASLDPANPPARLAEMLADCRAS
LALTSSQASHKLTAAPCPVHLVQDGACAPSTHIPLVSRPDDLAYVLFTSGSTGTPKGVCVRHA
SLSRLVSFLHLRLDLSPSDRWTQVASSGFDASVYEIWTPLACGAALLLADDDALRSPTALVSW
LVAQRATLSFMPTPLAEACFEQDWTGSALRAMTVGGDKLHPLRRPPFRLFNMYGPTEATVITT
VAEIADLGAEPPLGRPVDSALVYVLDPHMQPVPPGALGELYIGGACLAQGYTRTDLTAERFLP
DPFGQPGARLYRTGDLVRWRPDGQLAFAGRRDEQVKLRGRRVELGEVESVLRRLPGVREGIVV
LHGQGSAAHLIAHVVPDAHPPSERDLREGMARLVPDALVPAHFVLLPALPMSLSGKVDKKLLP
APPAAHADYEPPSGELELELAHIWQSVLHLDRVGRHDSFFDLGGHSLLAMQVLGRIESSLGIR

TTLRTLFEHPTLAQLASHLSSGAASTSAAAATALERGLTRPDGPSSPRVATPEEPFALTEGQR
AMWLECQKSADG
ALYNLGRTVRLGAGVDVAALRRAFEGLVERHEALRTTFLTRDGHPLQQVHRHVALEWAEEPAM
ALDEREIVARADEVRRRAFDLERGPLLRVHVWRRGEGQPPLLTVVVHHLVVDYWSFALLVREL
GELYSALRAGRPPQLPPPSSFFAAGVSCPSPREAAGGAEYWRKALDGATTAIDLPRDRARHDA
SPRRGRAHAITLPKPLTGALARLARERGTTLFSVLLSALTVLLHRASGQNDLVVGVPSAGRND
DESTRAFGYFVQMLPVRVALRGAASFDALVARVRDAFLDGLAHGDSALQHLLAEPRGAARRGG
ALFDVAFAFQGALPSLDPRLAALTTGAEDVRIAQGELELTTLADEQAAAEFDLALFAAELDSG
IALRFEYDQQLFDPATIERMARHFVLLLESAVEHPGRPLSELRMLSDAERALLLDDWSGAAAA
RQAASAPAPACVHALFEAHAARQPDATALEFGHQRFTYAELSTWSTELALWLRDRGVGPGSVV
GVCIERSPRMVAAQLAVLKAGAAYASLDPANPPARLAEMLADCRAALVLTSSQASHKLTAAPC
PVHLVQDGACAPSTHIPLVSRPDDLAYVLFTSGSSGTPKGVCVRHASLSRLVSFFQHLLALSP
RDRWTQLASSGFDASVYEIWTPLACGAALLLADDDALRSPTALVSWLVAQRATLSFMPTPLAE
ACFEQDWTGIALRAMTVGGDKLHPLRRPLPFRLFNMYGPTEATVITTVAEVADLGDEPPLGRP
IDSALVYVLDPHMQPVPPGVLGELYIGGACLAQGYTRTDLTAERFLPDPFGQPGARLYRTGDL
VRWRPDGQLAFAGRRDEQVKLRGRRVELGEVESALRRLPAVREGVVVLHGQGSAARLIAYVVP
GADPPSERDLREGMARLVPDALVPAHFVLLPALPMSLSGKVDKKLLPAPPAAHADYEPPSGEL
ERELAHIWQSVLHLDRVGRHDSFFDLGGHSLLAMQVLGRIESSLGIRTTLRTLFEHPTLHQLA
DRLSSGAASTTAAAATVPASEIAPSLGRAPAD
EPYPLSYEQERLWVLEQLLPGGTAYNVVQAVRLRNLVDVDALSSALAALVRRHWSLRTVFVAS
PTPQKICEPEAAPAEVVDLRGTPPDEAEAAARAWASREQATGFDLARGPVFRARLFRLDHDVC
VLVLSTHHIVTDAWSFQPLVRDLAELYRRARGGGPADMPELPLQYVDFAVWQRRHLAGKRLAD
KLAHWTATLRGLPVLELQTDRPRPPVQTFRGAERVLPLDARLVAQLDELARSRGATRFMVLLA
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LEAFEHQDAPFEKVVEAVNPRRDLSRSPLFQVMLVVQNAPTEALELGEVRIEPLDLPVEATRF
DLRFSVEPRGGRDVISLQYNVDLFDAATIDRMLATMQSVLSRATQDPAQRVRALSVAPEDRER
ALVAWNDTAVATPDHLRLEEPFFERAVEQPDACAVVDAERRLTYGELARRAEAIAAAASRSGA
TANALVAVVMEKGWEQVAAVLGVLRAGAAYLPLDPRLPEERLRHLLEHAEVRLVLTQSAVDGT
IAWPAGIERLAVDADERWREQPVARRPPGGSTDDLAYVIYTSGSTGLPKGVMIDHRGAVNTVL
DINRRFDVGPEDRVLALSSLSFDLSVYDVFGTLAAGGAVVIPDRTRASDPGHWRELVERERVT

VWNSVPALMEMLMDASPGAGDPALSSLRLVMMSGDWIPLKLPDRIRAACRAPRVVSLGGATEA
SIWSIAHPIADVDPAWRSIPYGRPLANQHTYVLDEGLEPCPIGVPGEIHIGGIGVALGYWRDE
ARTRERFLKHPTTGERLYRTGDLGRYFADGTIELLGRTDHQVKIRGFRIELGEIEAALAQHPS
VEQAVVAAKTDPSGEKRLVAYVVGADGDGAALRDFVRKKLPEYMIPAEVVVLPALPLSANGKV
DRAALPDPAAVAPRAAAVAPRTATERLIASVLAEVLQVEAVGVTDNLFELGFTSLLLVRAQRL
LAERIAARAPDEGAAAQAVSLTDLFQYPTIEQLAQRLDAATVKAEPADVGAQRAEARRDARRR
RGRG

SEQ ID No 110 (Contig 12 >ORF1)
PPAVRRYVADRRPEQLPALAPEEREAAARRLSALGAAPPQVRRRGLTRAPLSYGQSRIYFLEQ
LSPGKPLFNVPGAVRLRGPVDVARLSAAFGEIVRRHDALRTSIANVDGELLQIAQPHAGFALD
VVTSTPEEAAELDRRLRAEAWRPFAIGAPPLLRATLFRLAEDEHVLLVTMHHVVSDDWSLGVI
LRELLALYAGRSLPPPRLQVSDFAAWQREMVESGALDGQRAYWRERLRGLSRASISAGGGAEA
PSHDPSGAIEEIALSPDKAAALEALARREGATLFMVLLALLDLVIHARSGALDIAVGTPIANR
NRPELEDVVGLLTNTLVIRVDLARAGAFRDVLARARVQALDAFANQDIPFDVVTQDLKQERDH
AQHPLFRVWLALQNAPKPALEVRGLRVEPLPLRPELVHFEVALLLWPADDGSVVGHFEFRRDR
VDEGARKEIAAAFTHLVDAVIARPDAPVSTLVEGARAEAARAQAALGEAFARAATARLGQLRR
RSAGDRTPRE

SEQ ID No 111 (Contig 12 >ORF2)
MSIHIEEEGRADAAKAPPFDYLQALHSALAHENDPVKRKQIEAGMVFKWLREEPLPFLSQLRR
EKPIFSIPAITLVTRYNDVVEVLNANDVFSVDNIAPKLVENVGQNILAMNDSPKYEHEKSLLR
LAFPRADLPRYRQIVVDEANRLLAKVGVDKPFDLTGDYALRVPAGAMARYLGVGEIPTEKVVA
WTHALFNEIFLNPTNDPTAVAAARAARQEALPMIDAIVAARKKQLAKSPPPEQPSVLDRYLVM
QSVPETYESDEGIRDVILGLLMGCVDLSGGAIVNALVELMKRPRVLRDALNVVNVEDDAAITG
YVLEALRFRPPSTGVTSLCVRDYTVGRGTRHEEKVPAGALVMACSASAMHDHEHIDAPDQFRP
GRLPSRNYLFWESGIHTCHGKYVAILHISLAIKQLLRAGVPSAIDPMPRVHGYPAPFRVRLAA
AEG

SEQ ID No 112 (Contig 12 >ORF3)

MREPSSTPNWRNFGSNLPAGSDSVPPGEGFPIKKILALNLGKWKDTAGLQIAQALHLFEYGYK
RYREGKFVLRATSDLGLGAIFESIDNWESFDQFEEFFKPWTFIRKPLVATRWAEDAEFGRQRL
VGINPAHIRRATPADLADFVSGAEPKPIAIADGRTLEEVREGGQLYFLDYRIFKDIVDTDVQE
ELGKYPLAPTCMLHQTAAGELLPVAIRLVHSRPGKGAHPDKIFTPSGPSDDWLTAKIAVASAD
AIYQGQVTHLLYAHLIVEPFAVSTYRNLPATHPLHQLLRPHFFNTLAINELARRRFLGRGRFF
DITSSVATMGSFELLTRAYTGKGIKGYGGKPWRFYESALPRDLSARDVRDLVGYHYRDDALLH
WDAIQEYVGQVLKIAYPTPGSLSSDASLQRWIHELVSPQLGGMDSLLPPERADQLEKLTSLDD
LIAIVTNIIFTATAYHAAVNFGQTDYYTWIPNAQFATYRSYGDVLNGSEKRQFKPLERLPGRA
QSIRQMVLSRSLSMGPPLTSESLMTMKCLLQDPAAKQAFARYRERLAHIEREITERNRAREQP
YLYLLPSMVPQSVAI

SEQ ID No 113 (Contig 12 >ORF4)

VSSSRSTGRVPRDRASPAGSCAPALVPGPPLSYASVMPPLDLHVALFGASGAGKTVLLAAFYR
AQTQPSFQQEYAYKIQAVNKAQGNQLLGRFYRLEEGRFPDGSTRFDEYEFDFFPRDLPEPAVR
IHWYDYPGRWWEDEPVDADEREAMRQGLIRLGMSQVGILLADGAKYRAEGTGYIRWLFEHFAD
ECDRLRRASAATGDEVSFPREWILALSKADLCPPDYSARDFEREVCRDADDQLAKLCSVLRAE
HAFGHRFMLLSSVAAPAGAQVDPRTSLGVRTLAPAILVSTVEGAVREAQAARKEKSAGETFFQ
GLRDLVQFVDSLDDFLPKRYQIVSKILRFISIKDFATTRLDRLKKMREDAIRKGDTFTAVLTA
MVAALRDDEGARAYHQNQ

SEQ ID No 114 (Contig 12 >ORF5)

MPAPAPLVETSRLLWRTRGEHWDYEFICVPEIPALPAWLSTLEAMLADADAGAGELRYGLLEI
DDRGQRAPRAYPYVAVRFLDPARRDWTGRQVQHFAAWFPPVPPEAVAELPEAVPADWHLRVLD
GLAGTYGSGEVFGLPEATIRAWKRSHDESRAARAMAIVKATPPVSLGGGEAAPSRWTRVPTLK
KKPPEPPAAAGLLSVGAVPSGQGRRFGCFAIGAMMLAAFCRLMLACGVRLLGA

SEQ ID No 115 (Contig 12 >ORF6)

VRFRSSLGPLLLAALGAALTVSAAPRSAEASVFDSASRWPEDADGHVRIPVCIDPTSSAEQRV
DGAAGGLIHAPNPSLADVITRVRTALQGSWERWSSVRFTGWESCDSLLPATRMTYVGVRIHPD

APNQSDSIGVYNKGGSVQFKPWGADFNRCIKYNWQTARVEYSFDCVEQYAIHEMGHAIGFMHE
WHHPLVPSACSQREPLPASDVASGWPSSRRYIVVNPGFYDYDSIMTYWSGCSDQDGVRFGSET
LDAVDIQAVATVYPPVGGAPDVCNPGWFAGKRWFCAAQPTVSVGNSCSSGWVECLPHCNPRPF
QGEWWTCPTNPYAVTGQSCSARWELCGD

SEQ ID No 116 (Contig 12 >ORF7)
VGESQGALVGGNALSTNALNLNALNLNALNLNALNLSGLSARNLAAIQDPGPSGALARDFLRY
AASCALSSTASFDFSWTDSNGKRHDERYPGLLGVAPAWASGPLDDAGQRIVSSCVAARVNYYQ
VPVLLSARSLRDPLKTLSSSQELIDYPDVEGAFWGNLFAAQPYINACYNSATVDNSRAYQRDC
AAGHVTSGGQIVECGLIRIAGSCDRVCQKLNGAGQYYPSCVDRPGQSTATTKDVITTALP

SEQ ID No 117 (Contig 12 >ORF8)
VLAAHCERGGLTARAASLLARGAELAAARRAYLDAEGCYGRVEALLGALLPEERRARGLARFR
LGRHTEALADLAAAREAAAAASEAGAEIELLLDEAMILDWTGEYRAARERVAAAERLAGRVAS
PLLGARLLLGVGRSLHRADREDEAAAVLTRAAAQAARLGDEGHETHIIALLLLGFILASLGRV
EEAARDLDAVILSCEERSDLMHLGAALNNRGLARALQGDRAGMIADFERTIALGRELGQPAFE
LVGRYNLAEYLYLMDDLAAARPHARAVQAIAPRCGDRHAPVVVTLLIARLRLYQGDEAGARRI
ALRLRAARDDAGCEALKPSEDVLCAMIELATRDDDRAAWAALEERSARCSVGQERIEVLEARA
LAALRRGRRADARAQLERALAAASTIPTVMGGRLRRWYAELTRATESDAPDIDLAAAEATFTG
ARAREKVEY

SEQ ID No 118 (Contig 12 >ORF9)
QAYPDLWAERGRQELWLRQLPPRACAQLAREALGDAADGALIDRLVTQSEGQPFFLEELIRAT
AEGRGDALPETVVAMVQVRLEALAPPARRILRAASVLGEVFWRGAVAHLLGGDEAAPLAEHLS
ALVAGELCVRHREGRFPGEEEYSFRQALLREGAYAQLTKDDRALGHRLAADWLEAAGEADPLV
LAAHCERGGLTARAASLLARGAELAAARRAYLDAEGCYGRVEALLGALLPEERRARGLARFRL
GRHTEALADLAAAREAAAAASEAGAEIELLLDEAMILDWTGEYRAARERVAAAERLAGRVASP
LLGARLLLGVGRSLHRADREDEAAAVLTRAAAQAARLGDEGHETHIIALLLLGFILASLGRVE
EAARDLDAVILSCEERSDLMHLGAALNNRGLARALQGDRAGMIADFERTIALGRELGQPAFEL
VGRYNLAEYLYLMDDLAAARPHARAVQAIAPRCGDRHAPVVVTLLIARLRLYQGDEAGARRIA

LRLRAARDDAGCEALKPSEDVLCAMIELATRDDDRAAWAALEERSARCSVGQERIEVLEARAL
AALRRGRRADARAQLERALAAASTIPTVMGGRLRRWYAELTRATESDAPDIDLAAAEATFTGA
RAREKVEY

14. DNA sequence according to any of claims 1 to 5 wherein the DNA is selected from the group consisting of

(a) the following DNA sequences:

Seq ID No 119 (>Contig17)

TTACGTTACTCATCCTATCTCGGCACCCTGTGTCGGTGATGTCGCTCGCC
TCGAGCGCGAGCGGGACGACGTCGGCGCCGCGCTCGGTGAGCGCCGCCGC
GAGGGCGCTCGCGAGATCGCTGGCGACGCCGGCCGGGGCCACGACGAGCC
ACGTCCCCGCGACGTCGCCGCGTGACGCGGCGCTCACGGGTCTCCATTCG
ACGCGGTAGCGCCACGCGCCCACGGTGCTCTGCTCTCGGCGGCTCCGCCG
CCACGCCGACAGGGCCGGCATGAGGCTCTCGAGGGCCGAGCGCCGCCCGC
TGTCGGCGACGTGGAGCGCGTCCGAGAGCGCCGCGACGTCGCCGCGCTCG
ATGGCTCGCCAGAACGCGGTCTCCTCGGCGGACGCTCCCGGCGCCGCGTC
CTCATCGTCCGACGCGTCGCCTGCGTCGAGCCAGAACCGCTCGCGCTGGA
ACGCGTACGTCGGCAACGTCACGCGGCGCGCCCCGAGCGGAGCGAAGAAC
GCACCCCAGTCGATGGCGTGCCCGCGCGCGTGGAGCTCGCCTGCCGAGAG
GAGGAAGCGCTCGAGGTCGCCTTCGTCGCGGCGGAGCGAGGACACCACGG
TCGCATCGCCGTCGATCGACGAGAGCGTCTCGTCGAGCGCGACGGTGAGC
ACGGGGTGAGGGCTGACCTCGACGAAGAAGCGGTGGCCGTCGTCGAGCAG
GGCGCGCGTGGCGTGCTCGAAGCGGACGGTGTGGCGCAGGTTTCGGTACC
AGTGGGCGGCGCCGAGGGCCTCGCCATCAAGCCTCTCGCCCGTCACCGCG
GAGTAGAGCGGCACGGTCGCCGGGCGCGGCGCGATGCCGTCGAGCGCCTC
CAGCATCGTCCGCTCGATGGCCTCCACGTGGGCGGAGTGGGAGGCGTACT
CGACGCGGACCTTGCGGGCGAACAGCTGCGCCCCGCTCAGCTCTGCGACG
AGCTCGTCGATAGCGCCGGGGTCTCCGGAGACGAGGGCCGCGTGAGGGCT

GTTGATCGCCGCTATCGCCAGGCGTTCGCCCAAGGGCGCAAGGCGCGCCT
CGAGCTCGGCGGTGGTGAGCTCGACGGCGGACATGGCGCCGCGTCCCGCG
AGCTTCGTAATGGCGCGCGAGCGGAGCGCGACGACCCTGGCGGCGTCTTC
TAGCGAGAGCGCGCCCGCGACGTACGCGGCCGCGATCTCGCCCTGGCTGT
GGCCGACGACCGCGTCGGGCGTGACTCCGGCGGCGCGCCAGGTGGCGGCG
AGGGCGATCATGACGGCGAACAGCACGGGCTGCACCACGTCGACGCGCTC
GAGCATGGGCGCGGCGTGCGCTTCGTCGCCGCCGAGCACGGCGAGGAGCG
ACCAGTCGACGTGCGGCGCCAGGGCGCGCTCGCACGCCTCGATCTCGGCC
CGAAAGGCGGGCGAGGAGGCGAGCAGAGCGCGCGCCATCGATGGCCACTG
CGAGCCCTGGCCGGGGAAGACGAAGGCGACCTTGCCCGGCGGGAGCGCCT
CGCCCGCGACCGTTCCTGCCCCCGCGCGCCCCTCGGCGAGCGCCGCGAGC
GCCGAGAGCAGCGCGGCGCGATCGTCTGCCACGACGGCGGCGCGACGCTC
GAAATGCGACCGCGTGGTCGCGAGCGACGCCGCGACGTCGACGAGGGCGA
CGTCCTCGTGCTCGGCGAGGTGCGCGTGGAGCTTGCCCGCCTGAGCGCGG
AGCGCCGCGTCGCTCTTCGCCGAGAGGAGCACCGGCACCGGCGGCGCGAA
GGGCGCGCGGGCGGGCTCCCCGGCCTGGTCGTCGCCGGCCGCCGCGCGCG
GCGCTTCCTCGAGGACCACGTGCGCGTTGGTGCCGGAGATCCCGAACGAC
GACACCGCCGCGCGCCGAGGAGACCCGCCTGGCTTCCACGGTACCTCCTC
GGTCAAGAGGCGGATCGCGCCGGACGACCAATCGATGTGCTGCGACGGGC
TCGCGGCGTGGAGCGTCCTCGGGAGGACGCCGCTCTGCAGCGCGAGCACC
ATCTTGATGACGCCGCCGATCCCCGCGGCGGCCTGCGTGTGCCCGAGGTT
CGACTTTAGGCTCCCGAGCCACAGCGGGCGCTCCTTCGCGTGCGCCGCGC
CGTACGTCGCGAAGAGCGCGCGCGCCTCGATGGGATCGCCGAGCGTCGTG
CCGGTTCCGTGCGCCTCGACGGCGTCGACGTCCGCGGGGGCGAGCCCCGC
GCTCGCGAGCGCGTCCCGGATCACGCGCTCTTGCGCGGGGCCGTTCGGCG
CCGTGAGCCCTTGGCTCTTGCCGTCCTGGTTGACGGCCGATCCGCGCACG
ATCGCGAGCACGGGGTGCCCGTTCTTCCGGGCGTCCGACAGGCGCTCGAG
GAGCACTATCCCAGCGCCTTCCGACCAGCCCGCGCCGTTCGCGTGCGACG
AGAACGACTTGCACCGCCCGTCCGGCGCGCCCGCGTGCTGCGCGCTGAAC
TCGCCGAAGATCCCGGGGGTCGCCATCACGGTCACGCCGCCGGCGAGCGC

GAGCGAGCACTCGCCTCGACGGATGGCGTGGCAGGCGAGGTGGAGCGCGA
CGAGCGACGAGCTGCACGCCGTGTCGACGCT

Seq ID No 120 (>Contig18)

TTTTAGGANCCCCGACGTGCACGATCGGCTCGCCAACCTCGTGGCGCGCC
GGGACTATTTTTACCAGCTCGCGTTGCGCGCCGCGGGGACCTACGTGCGG
GGCCTCGTCCGCGCCCCGCACGACGGCGCGCGCCCCCCCGCGTTCGCGCC
GCGTGGGGCGGCGCTCGTCACGGGCGGGACCGGGGCGCTCGGGGCGCACG
TTGCCCGTTGGTTCGCGCGGATCGGCGCCGAGCACATCGTGCTCGCGAGC
CGCCGCGGAGCCGCGGCCCCCGGCGCGGCCGCGCTCGCCGAGGAGCTTTC
GGTGCTCGGCGCGCGCGTGACGCTGGTTGCGTGCGACGTCCCCGATCGTG
AGGCGGTCGCGGGGCTCGTGCGCAACGTCAAGGCCGGCGGAGCGACGGTG
CGCGCCGTGTTCCACGCGGGCGGTGCGATGCACGAGGCGCCGGTCGCCGC
CATGCGTGTTGAGGAGCTCGCCGACGCGATCGCCGTGAAGGCCCGCGGCG
CGCAGCACCTCCAAGACGTCTTCGCGCAGCGCCCGCTCAACGCGTTTGTC
CTCTTCTCGTCAGAAACGGGTGTGTGGGGCGGTGGCCGGCAAGGCGCGTA
CGCCGCGGCGAACGCGTTCCTCGACGCGCTCGCCGAGGCGCGTCGCGCGG
ACGGCCTCGCGGCGACCTCGATCGCGTGGGCGCGTGGGCGGGCGGCGGA
ATGCTCGCGACCGACGCCGAGCGGCGCTTGAAGCATCGCGGCGTCGCGCC
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CCGAGACGTGCCTCGCCGTCGCTGACGTCGACTGGGCGCGCTTCGCCCCG
TCGTTCGCCTCGGCGCGTCCTCGCCCGCTCCTCGACGAGCTCGCGGAGGC
GCGATCGGCGCTCGACGCGCTGCGCGAGCCACCGGACGACGCGCGCACGG
CCGCCGGTCCCGAGCCCGCAAGCACGCTGAGGACCACGCTCGCGGCGCTC
CCGGAGGGCGAGCGCCACCGCCACCTCCTCGCGCTCGTGCGGACGGAGAC
GGCGGCGGTGCTCGGGCACGCGGACGCGTCGCGCGTCGAGCCGAACCGCG
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CGCGTCCAGCGCGCGACCGGCATCAAGCTCCCGGCGACGCTCGCGTTCGA
CCACCCGACGCCGAGCGCGCTCGCGAGCAAGGTGCTCGCCGCGATCGTCC
TCCACGACGCGACCCCGCGCGCCTCGCCCGCCGCGGAGCTCGAGCGCCTC

GAGGGGATGCTCTCGGCGATCTACGCGGACGAAGCGCTCCGCGACGACCT
CACGGCGCGCCTCCGCGCCTTCCTGGACAAGCGCGCGGTCCGCACCGAAC
GCCCCGACGACGCCGCGTTCGCCGAGAAGCTCGGCTCCGCGAGCGCCGAC
GAACTCATTCGCCTGATCGATCAGAAGCTCGGAGATCGCATCGATGTCGA
CCGTTACTAACGACACGCTCACGGAGTACTTGCGGCGCCTCACTCAAGAG
CTCCACAGGAGCGAGACGCGCCTGCGTGCGACGGAAGAGAGGCGACATGA
GCCGATCGCCATCGTCGGCCTCGGGCTCCCCTTCCGGGGCGGGATCCACG
ACCGCGACACGCTCTGGACGTTCCTCGAGGAGGGCCGCGACGCCATCGCG
CCGATCCTCGCGAGCCGCTGGAACGCGGACGCGACGTACGACCTCGATCC
GGACGCCGTCGGCAAGAGCTACGTGCGCGACGCCGCCATGCTCGATCGCG
TCGACCTTTTCGACGCCGATTTCTTCGGGATCAGCCCGCGCGAGGCGAAG
TACGTCGACCCGCAGCACCGCCTCTTGCTCGAGACGTCGTGGCAAGCGCT
CGAGGACGCGGGGATTGTGCCGGCGTCGCTGCGAGACTCGAAGACCGGCG
TCTTCGTCGGCACGGGCGCGAGCGACTACGCGTTCCTCCAGAGCGATCGC
GACGCCTCGGAGGCGTACGCGTTCATGGGGATGATCTCGTCGTTCGCGGC
GGGCCGCCTCGCGTTCACGCTCGGGCTCCAAGGCCCCGCGCTATCGATCG
ACACGGCGTGCTCTTCGTCGCTCGTCGCGCTCCACCTCGCGTGCCAGTCG
CTGCGTCAAGGCGAGTGCGACCTCGCGCTCGTCGCGGGTGTGCAGGTCAT
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GCGACGGGCGATCGAAGACGTTCTCGGCGAACGCCGACGGCTATGGCCGC
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ACGGCACGTCGAGCGGGATCACGGTCCCGAACGGGCCCGCGCAGCAGAAG
GTGCTCCGCGCCGCGCTCGACGACGCGCGGCTTGTCCCCGCCGACGTCGA
CGTCGTCGAGTGCCACGGCACGGGGACCTCCATCGGCGATCCCATCGAAG
TGAACGCGCTCGCCGCCGTCTACGGCGAGGGGCGCCCCAAGGACCGCCCG
CTGTTCCTGGGCGCGCTGAAGACCAACATCGGGCACCTCGAGTTCGCGTC
GGGCCTCGCCGGCGTCGCGAAGATGGTCGCCTCCATGCGCCACGCGACCC
TCCCCGCGACGCTGCACACGAGCCCGCTCAACCCGCTCGTCGACTGGGAC
GCGCTCCCCGTGCGCGTCGTCGACGCCGCGCGCCCGTGGACGCGCCGCGA

CGACGGCGCCCCCCGGCGCGCCGGCGTCACGGCGATCGTCGAGGAGGCGC
CCGCCGAGCCCGAGCCCACGACGCCCGACGCCGCGCCCGCGCTTCCGGCC
GTGCCCGTTCTCCTCTCGGGCAAGACCGACGAGGCGCTGCGCGCGCAGGC
AGCGCGCCTCCACGCGCACCTCGCGGGGCGCCCCGACGCGCGGCTCGTCG
ACATCGCCGCGTCGCTCGCGACGACGCGCACGCACTTCGATCGACGCGCG
GCCGTCGTCGCGGCGGATCGCGACGAGCTCCTCGGCGCGCTCGACGCGCT
CGCGCGCGGCGAGGCAGGCCCGGGGTCGGTCGTCGCGAGCGCGATCCCCG
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TCGCCGCCGCCTACGTCGCCGGCGCCCTCTCGCTCGAAGACGCCGCCAAG
GTCGTCGCGCTGCGCGCACGAGCGCTCACGAAGATCGCGGGGCGCGGGGC
GATGGCCGCCGTCGAGCTCGGCGCACGCGACACCGAGGCGCGCCTCGCGC
CGTTCGGCGACGCCATCGCGATCGCGGCGATCAACAGCCCGCGCGCCACG
CTCGTCGCGGGCGACACGGACGCGATCGACGCGCTCGTCCGCGACCTCGA
GGCCGCGCAGATCTTCGCGCGGAAGGTGCGTGTCGACTACGCGTCGCACT
CGGCGCACGTCGAGGCGATCGAGCGCGAGCTCCTCGCGGATCTCGCGGGG
ATCGAACCGCGCGCGGGCGCTGTGCCGCTTTACTCCGCGGTGACGGGCGC
GAAGCTCGACGGGAACCGCCTCGACCCCGCGCATTGGTTCCGGAACCTGC
GCTCGACAAAAAACTTTGAGGACGCCACGCGCGCGCTCCACGACGACGGC
CGCCGGGTATCCTCATNATCNNGGGCGTNCAGAGGAGTCGGTATTNCCCC
CCCCCGCCTTNCCCG,

or their complementary strands,

(b) DNA-sequences which hybridise under stringent conditions to regions of DNA-sequences according to (a) encoding proteins or to fragments of said DNA-sequences,

(c) DNA-sequences which hybridise to the DNA-sequences according to (a) and (b) because of a degeneration of the genetic code,

(d) allele variations and mutants resulting by substitution, insertion or deletion of nucleotides or inversion of nucleotide segments of DNA-sequences according to (a) to (c), wherein the variations and mutants offer isofunctional expression products.

15. Peptide encoded by a DNA sequence according to claim 14 selected from the group consisting of

Seq ID No 121
>Contig17_001 828 amino acids MW=86259 D pI=5.60 numambig=1
MTVMATPGIFGEFSAQHAGAPDGRCKSFSSHANGAGWSEGAGIVLLERLSDARKNGHPVL
AIVRGSAVNQDGKSQGLTAPNGPAQERVIRDALASAGLAPADVDAVEAHGTGTTLGDPIE
ARALFATYGAAHAKERPLWLGSLKSNLGHTQAAAGIGGVIKMVLALQSGVLPRTLHAASP
SQHIDWSSGAIRLLTEEVPWKPGGSPRRAAVSSFGISGTNAHVVLEEAPRAAAGDDQAGE
PARAPFAPPVPVLLSAKSDAALRAQAGKLHAHLAEHEDVALVDVAASLATTRSHFERRAA
VVADDRAALLSALAALAEGRAGAGTVAGEALPPGKVAFVFPGQGSQWPSMARALLASSPA
FRAEIEACERALAPHVDWSLLAVLGGDEAHAAPMLERVDVVQPVLFAVMIALAATWRAAG
VTPDAVVGHSQGEIAAAYVAGALSLEDAARVVALRSRAITKLAGRGAMSAVELTTAELEA
RLAPLGERLAIAAINSPHAALVSGDPGAIDELVAELSGAQLFARKVRVEYASHSAHVEAI
ERTMLEALDGIAPRPATVPLYSAVTGERLDGEALGAAHWYRNLRHTVRFEHATRALLDDG
HRFFVEVSPHPVLTVALDETLSSIDGDATVVSSLRRDEGDLERFLLSAGELHARGHAIDW
GAFFAPLGARRVTLPTYAFQRERFWLDAGDASDDEDAAPGASAEETAFWRAIERGDVAAL

SDALHVADSGRRSALESLMPALSAWRRSRREQSTVGAWRYRVEWRPVSAASRGDVAGTWL
VVAPAGVASDLASALAAALTERGADVVPLALEASDITDTGCRDRMSNVX

Seq ID No 122
>Contig18_002 502 amino acids MW=53019 D pI=6.83 numambig=1
FRXPDVHDRLANLVARRDYFYQLALRAAGTYVRGLVRAPHDGARPPAFAPRGAALVTGGT
GALGAHVARWFARIGAEHIVLASRRGAAAPGAAALAEELSVLGARVTLVACDVPDREAVA
GLVRNVKAGGATVRAVFHAGGAMHEAPVAAMRVEELADAIAVKARGAQHLQDVFAQRPLN
AFVLFSSETGVWGGGRQGAYAAANAFLDALAEARRADGLAATSIAWGAWAGGGMLATDAE
RRLKHRGVAPMDPELAVAALAHALDHAETCLAVADVDWARFAPSFASARPRPLLDELAEA
RSALDALREPPDDARTAAGPEPASTLRTTLAALPEGERHRHLLALVRTETAAVLGHADAS
RVEPNRGFFDLGLDSLMSVELRRRVQRATGIKLPATLAFDHPTPSALASKVLAAIVLHDA
TPRASPAAELERLEGMLSAIYADEALRDDLTARLRAFLDKRAVRTERPDDAAFAEKLGSA
SADELIRLIDQKLGDRIDVDRY*

Seq ID No 123
>Contig18_010 840 amino acids MW=88062 D pI=5.74 numambig=6
MSTVTNDTLTEYLRRLTQELHRSETRLRATEERRHEPIAIVGLGLPFRGGIHDRDTLWTF
LEEGRDAIAPILASRWNADATYDLDPDAVGKSYVRDAAMLDRVDLFDADFFGISPREAKY
VDPQHRLLLETSWQALEDAGIVPASLRDSKTGVFVGTGASDYAFLQSDRDASEAYAFMGM
ISSFAAGRLAFTLGLQGPALSIDTACSSSLVALHLACQSLRQGECDLALVAGVQVMSSPE
VFVLLSRTRALASDGRSKTFSANADGYGRGEGVVVLAVERLRDARAKGRPILAVIRGSAV
NHDGTSSGITVPNGPAQQKVLRAALDDARLVPADVDVVECHGTGTSIGDPIEVNALAAVY
GEGRPKDRPLFLGALKTNIGHLEFASGLAGVAKMVASMRHATLPATLHTSPLNPLVDWDA
LPVRVVDAARPWTRRDDGAPRRAGVTAIVEEAPAEPEPTTPDAAPALPAVPVLLSGKTDE
ALRAQAARLHAHLAGRPDARLVDIAASLATTRTHFDRRAAVVAADRDELLGALDALARGE
AGPGSVVASAIPAGRVVFVFPGQGSQWVGMARALLASSVVFRDEIAACERALAPHVAWSL
GAVLRGDGDEATLLGRVDVVQPVLFAVMVALAALWRSIGVTPDAVVGHSQGEIAAAYVAG
ALSLEDAAKVVALRARALTKIAGRGAMAAVELGARDTEARLAPFGDAIAIAAINSPRATL
VAGDTDAIDALVRDLEAAQIFARKVRVDYASHSAHVEAIERELLADLAGIEPRAGAVPLY

SAVTGAKLDGNRLDPAHWFRNLRSTKNFEDATRALHDDGRRVSSXSXAXRGVGIXPPRLX
X

16. Recombinant expression vector which comprises a DNA-sequence according to any of claims 1 to 10, 12 and 14.

17. Procaryotic or eucaryotic cell which has been transfected or transformed with a DNA-sequence according to any of claims 1 to 10, 12 and 14 or with a recombinant expression vector according to claim 16.

18. Cell according to claim 17, wherein the cell is derived from myxobacteria.

19. Cell according to claim 17, wherein the cell is derived from a Sorangium strain.

20. Cell according to claim 17, wherein the cell is derived from Sorangium cellulosum.

21. Cell according to claim 17, wherein the cell is derived from a Streptomyces strain.

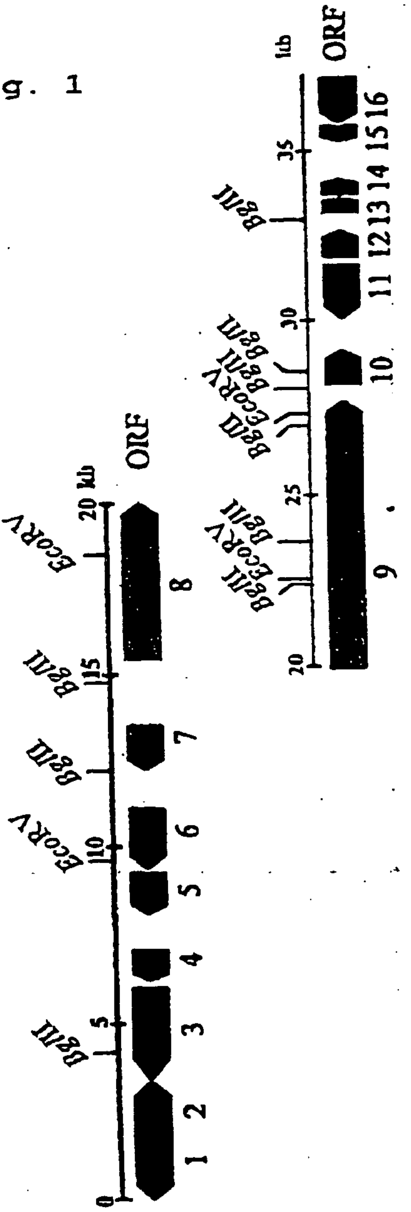
22. Cell according to claim 17, wherein the cell is derived from Escherichia coli.

23. Process for an enzymatic biosynthesis, mutasynthesis or partial synthesis of polyketide or heteropolyketide compounds, wherein a cell according to any of claims 17 to 22 is culti-

vated in a suitable culture medium and the polyketide or heteropolyketide compound is isolated from the medium.

24. Process according to claim 23, wherein the polyketide or heteropolyketide compound is an epothilone.

Fig. 1


0
5
10
15
20 kb
ORF
BglII
EcoRV
BglII
BglII
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1
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16

Open reading frames found on pEPOcos6 region.

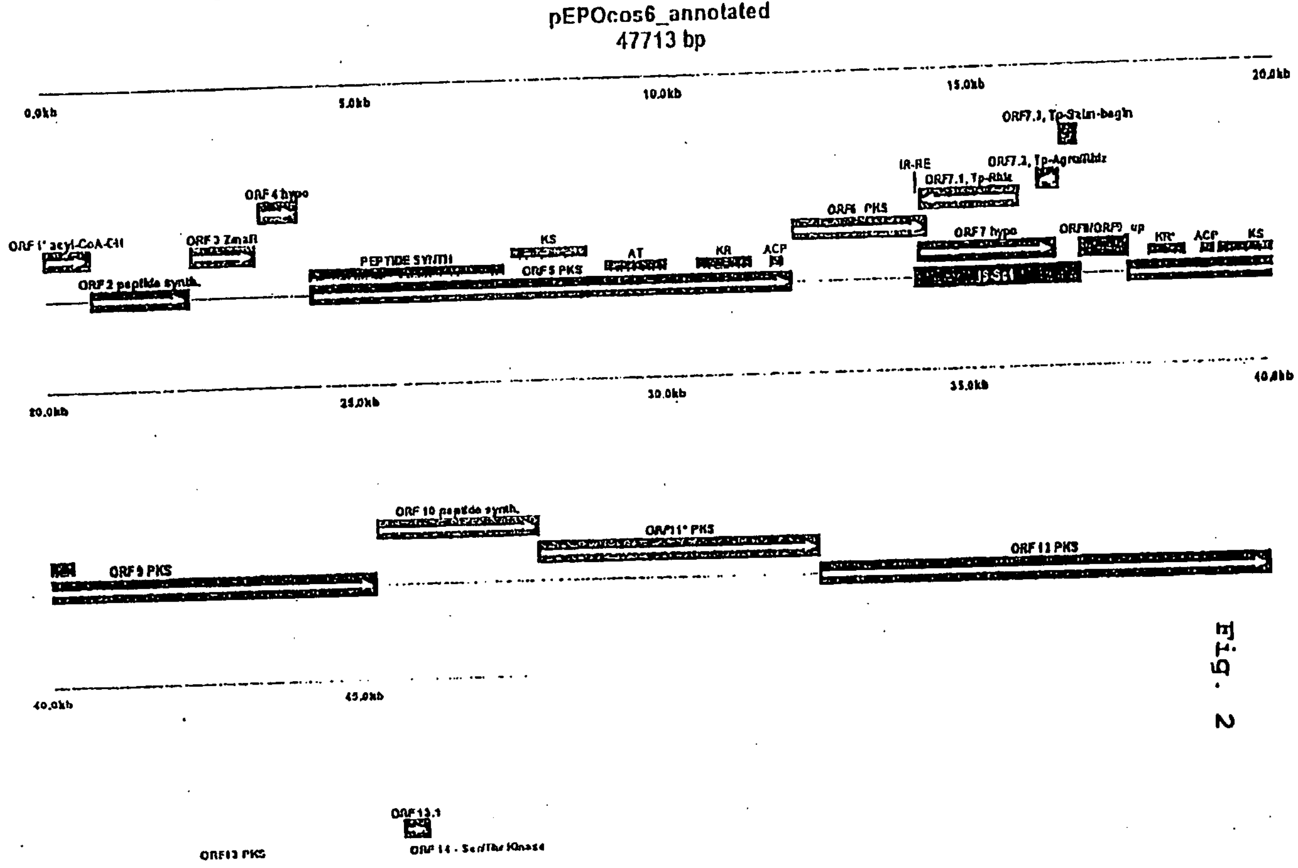

Fig. 2